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BCO51876 2655 bp mRNA linear HTC 05-MAY-2003
Homo sapiens cDNA clone IMAGE:6527736, containing frame-shift
                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2655)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITITITITICCICATATICACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGT
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                                                                                                                                    1479 AAACAGAATTAGGAGTIGIGGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACACAGAAAA
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                                                                                                                                                                                                                                                             1116 AAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAAGACAGAAAA
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AGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAASACCGGTGTCAGG
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                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: g Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186
This clone has the following problem: frame shifted.
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         Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
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Pred. No. 3.6e-286;
1; Mismatches 3;
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Corganism="Homo sapiens"
| Mol Lype="mRNA" |
| db xref="taxon:9606" |
| clone="IMAGB:4614150" |
| fissue -type="Kidney" |
| clone lib="NIH MGC 75" |
| lab host="DH10B"
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519 c 591 g 846
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Best Local Similarity 99.7%;
Matches 1497; Conservative
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         Klausner, R.D., Colling, F.S., Wagner, L., Shemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.B., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Morley, K.C., Malek, J.A., Gunaratne, P.H., Richards, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.H., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Bakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalka, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome
CA 94305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 110 Row: p Column: 4 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (01-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                           human and mouse CDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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Feingold, E.A., Grouse, L.H., Derge, J.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Uterus, leiomyosarcoma"
/clone lib="NIH MGC 71"
/lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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llarity 99.6%; Pred. No. 1.7e-285;
Conservative 1; Mismatches 2;
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479 c 551 g 803 t
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/db_xref="taxon:9606"
/clone="IMAGE:6527736"
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Strausberg, R.
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Matches 1495;
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ORIGIN
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
PUBMED
AUTHORS
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1086 1146 1206 967 CGCTGTGGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGTAATGTCAATGTGTCCCA 1026 1387 AGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTC 1446 935 635 755 275 395 455 999 726 786 695 906 486 909 907 ATAAGGGAAGGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCTCCTGGTTAAA 966 1027 AGCAAAGTTACTAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAGACGGGTGTCAGG GCAGTAGAGGAAAATGTATGGATACAACTTACGTTTGATGAAAGATTTGGGCTTGAAGAC 547 CAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCAGGGTTCTGCATC CACTACAACATGTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCT TCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAGAC TCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAGAC AACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCC GGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTG CAGTGCAGTGCCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT GTTTGCTTCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGAGACATC AAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAA AAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAA CCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACT ATATTAGGGCGCTGGTGTTGTTGTTACTGTACCAGGAAAACAGATTTCTAAAGGAAAT CAAATTAGGATAAGATTTGTATCTGATGAATATTTTTCCTTCTGAACCAGGGTTCTGCATC CTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCA ACTTGGCAACTTCTTGGCAAGGCTTTTTGTTTTTGGAAGAAAATCCAGAGTGGTGGATCTG 787 ACTTGGCAACTTCTTGGCAAGGCTTTTTTTTTGGAAGAAAATCCAGAGTGGTGGATCTG ATAAGGGAAGAACTAAAGAGAGACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAA AGCAAAGTTACTAAAAATACCACGAGGTCCTTCAGTTGAGACCAAASACCGGTGTCAGG TGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCCAGAGCTGTG CAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT GITTGCTTCAAGGACCTTTCATCTTCAGGATTTTACAGTGCATTCTGAAAGAGGAGACATC CCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACT ATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAAACAGATTTCTAAAGGAAAT CACTACAACATTGTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCCT AACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCTCAGTGTCC **AGGTCTTCAATCGTGGAAAGAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTTC** GCAGTAGAGGAAAATGTATGGATACAACTTACGTT

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969 bp mRNA linear EST 01-MAY-2001 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4750095 5',
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                                                                                                                                                                                                                                                                              171 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC 230
                                                                                                                                                                                                                                                                                                                                                                                                                           291 TTGTAGAAGTTGAGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTGTTGGTA 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCA-TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTT 780
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                         GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
                                                                                                                                                           GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC
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                                                                                                                                                                                                                                           CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC
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                                                                             4 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
                                     Gaps
                                     4.
DB 13; Length 999;
                                     Indels
Score 787.2; DB 13
Pred. No. 6.9e-147;
0; Mismatches 8;
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51.3%;
98.6%;
                  Best Local Similarity 98.6
Matches 826; Conservative
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mRNA sequence.
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Query Match
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VERSION
KEYWORDS
SOURCE
ORGANISM
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//db xref="mrRNA"
/db xref="mrRNA"
/db xref="mrRNA"
/db host="mrRNA"
/db host="mrRNA"
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/dlone lib="NIH MGC_121"
/dlone lib="NIH MGC_121"
/note="organ: brain; Vector: pCMV-SPORT6; site 1: Not1;
Site 2: Born (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (Ecory site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen) Research Genetics tracking code 017. Note: this is a NIH MGC Library.

90 a 213 c 235 g 261 t
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AGENCOURT_6794408 NIH_MGC_121 Homo sapiens cDNA clone IMAGB:5770510
                                                                                                                                                                                                                                                                                   1683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 999)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAM12833 row: k column: 23
High quality sequence stop: 676.
                                                                                                                                                                                                                                                                                                                         1476 TTTAAAAAGGAACTATGTTGCTATGAATTAAACTTGTGTCATGCTGATAGGACAGACTGG
                       AGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGC
                                                                                 TTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTT
                                                                                                      TTAGGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGGACCTGATTCCGTTGCCTT
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/organism="Homo sapiens"
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Harrington, J. (Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McBligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Zeration of gene expression libraries using random activation of gene expression
                                                                                                                                                                                                                                                                                             1397 AAAAICIGGATITITITITITITITITIGCICATATICACATATGIAACCAGAACATTICT 1456
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RST4916 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG185961
541 AAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTACCCACTGTTGTATTACAT
                                                                 601 AGALCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTT
                                                                                                                                                661 CAGTTCTTTCGATACGGCTTACGGTAATGTCAGTACAGGAAAAAACTGTGCAAGTGAGC
                                                                                                                                                                                                             1338 ACCTGATTCCGTTGCCTTGCTTAACTC-TAAAGCTCCATGTCCTGGGCCTAAAATCGTAT
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                                                                                                                            CAGTICITICGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGC
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Tel: 216 431 9900
Fax: 216 361 9596
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High quality sequence stop: 4
Location/Qualifiers
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                                           National institutes of Health, Mammalian Gene Collection (MGC)
Uppublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
Linkalofo4 row: f column: 16
High quality sequence stop: 764.
High quality sequence stop: 764.
Location/Qualifiers
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// mol type="MRNA"
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// clone="MRAGE:4750055"
// tissue_type="MRNA"
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// note="Organ: 8kin; Vector: pcMV-SPORT6; Site_I: Noti;
Site_2: Sali, Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library.

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                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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TAGCCGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTAT 1016
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/lab host="DH108 (T1 phage-resistant)"
/clone_libe="Not GAP Skrif"
/note="Organ: Skin; Vector: pCMV-SPORT6; Site_1: Not!;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                  Context: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Profurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10610 row: d column: 13
High quality sequence stop: 803.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BG681390
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Homo sapiens
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1142)
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1; Mismatches 17;
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Mus musculus 15 days embryo head cDNA, RIKEN full-length enriched library, clone:D930001M08 product:platelet-derived growth factor, C polypeptide, full insert sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
     GCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTT
                        GCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTT
                                                                          TCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGGGAACTGTGCCTGTTGTCTCCACA
                                                                                                                                              ATTGCAATGAATGTCAATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTC
                                                                                                                                                                                 ATTGCAATGAATGTCTATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTC
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                                                                                                 TCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12030 row: i column: 02

High quality sequence stop: 791.
TCTTCAGGATTTACAGTGCATTCTGAAAGAGGGAGACATCAAACAGAATTAGGAGTTGTGC
                                                                                                     702 rerreadgarriracagracarrerdaaagagagacarcaaacagaarraggagrage
                                                                                                                                          AACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGAGAAAGGTCTTC-AATCGTGGAAAG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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11 Similarity 97.6%; Pred. No. 4.7e-136;
786; Conservative 1; Mismatches 11:
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Homo sapiens
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Analysis of the mouse transcriptome based on functional annotation of 60,710 full-length cDNAs

I. Mature 420, 563-573 (2002)

E. (bases 1 to 2765)

S. Adachi, J., Alzawa, K., Akimura, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kono, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matuyama, T., Miyazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shibata, M., Shiba
prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                            Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sawai, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegani, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Warahiki, M., Voneda, Y., Ishikawa, T., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKSI nintegrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Direct Submission
Exploration Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
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Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Fax: 81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
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Nature 409 (6821), 685-690 (2001)
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/dev stage="15 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                               /note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD|MGI:1859631, GB|NM_019971, evidence: BLASIN, 99%, match=2691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC
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Pred. No. 9.6e-134;
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/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                        organism="Mus musculus"
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Kawai, J. Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Atakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Atakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Atakawa, M., Inshi, K., Kiyosawa, H., Komdo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasubawa, T., Yamanaka, I., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Kadota, K., Matsuda, H., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Furuno, M., Aono, H., Wagner, I., Washio, T., Sakai, K., Okido, I., Furuno, M., Aono, H., Eatcher, C., Pulta, M., Gariboldi, M., Gustinoich, S., Hill, D., Fletcher, C., Pulta, M., Gariboldi, M., Gustinoich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Narchiomi, L., Maszia, M., Lee, N. H., Lyons, P., Marchiomi, L., Maszia, M., Lee, N. H., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Toyo-oka, K., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y. Soshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. Runchonal annotation of a full-length mouse cDNA collection
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S Adachi, J., Azizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, K., Hayatsu, M., Hiraokt, T., Hiraoka, T., Hiraoka, T., Harai, M., Hiraoka, T., Harai, M., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itch, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kondo, S., Konno, H., Kaukawa, T., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Ohno, M., Okazaki, Y., Saito, R., Saito, H., Sakai, K., Ohno, M., Ohaato, N., Okazaki, Y., Saito, R., Saitoataki, T., Sakai, K., Sakai, Sak
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases I to 3244)
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Fax:81-45-503-9216)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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Genome Res. 10 (11), 1757-1771 (2000)
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/strain="C57BL/6J"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
   AIGCIGIGACTGCCTTCAGTACCTTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGAT
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HTC; CAP trapper.
Mus musculus (house mouse)
ACAGCTGCACACCCCGGAACTTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATA 1552
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Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                            CCATTITCIGGCCAGGITGICCCCGGTTAAACGCTGIGGTGGGAACTGIGCCTGITGIC
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High-efficiency full-length cDNA cloning
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                                                                                  /note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD|MGI:1859631, GB|NM_019971, evidence: BLASTN, 99%, match=2691)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

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Nature 420, 563-573 (2002)

E ( Dases I to 3405)

S Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Nakamira,K., Natih,K., Numaraki,R., Miyazaki,A., Murata,M., Nishi,K., Saitoh,H., Sakai,C., Sakai,K., Sakai,M., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Tarawa,T., Tanawa,T., Tomaru,A., Toya,T., Yasunishi,A., Muramateu,M. and Hayashizaki,Y.

Direct Submission Hayashizaki,Y.

Direct Submission Institute; 1-7-22 Suehiro-cho, Tsurumi, Fu, Yokohama, Kanagawa, 230-0045, Japan (E-mail:genome-res@ggc.riken.go.jp, Fax:81-45-503-9222, Prem. Pax.81-45-503-9222, Prem. Pax.81-45-503-9216)
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fretcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakonoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Wynshwa Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection but but a full-length mouse cDNA collection but a full-17851
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RHENUTISGGWGSTHGSPKPHTYPRMVLVWRLVANDENVRIQLFPDERFGLEDPEDD
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TWQLLGKAFLYGKKSKVVNLNLLKEEVKLXSCTPRNFSVSIREELRYTDIFWPGCLL
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Please visit our web site for further details.
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/dev_stage="7 days neonate"
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/db_xref="taxon:10090"
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URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                     4 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
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This clone was selected for full length sequencing because it
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GCCAGGITGTCTCCTGGITAAACGCTGTGGAGGGAACTGTGCCTGTTGTCTCCACAATTG 302
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Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trausberg, R. Direct Submission Direct Submission Submission Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.,
                                                                     CAATGAATGTCAATGTCCCAAGCAAAGTTACTAAAAAATACCATGAGGTCCTTCAGTT
                                                                                                                                     CCATGAGGAGTGTGACTGTGTGTGCAGAGGAGCACAGGAGGATAGCCGCATCACCACCA
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                                       CAATGAATGTCAATGTCCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTT
                                                                                                               GAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCA
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC029099 2893 bp mRNA linear HTC 2 Mus musculus, Similar to platelet-derived growth factor, polypeptide, clone IMAGE:3660797, mRNA. BC022099
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Center code: BCM-HGSC
Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly'
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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Contact: MGC help desk
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 2893)
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                                                                                                                                                                                                                                     Macaca mulatta (rhesus monkey)
Macaca mulatta
Macaca mulatta
Macaca mulatta
Macaca mulatta
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.

1 (bases 1 to 769)
NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NOI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
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                                       1811 AGCCTTCGTAGCAGCAC 1827
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passed the following selection criteria: matched mRNA gi: 10242384 This clone has the following problem: frame shifted. Location/Qualifiers
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                                                                                                                                                                                          /mol_type="mRNA"
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/clone="INAGE:3660797"
/tissue type="Manmary tumor metastatized to lung.
/mmrv-LTR/Wnt1 model. Expression driven by an MMTV-LTR
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Pred. No. 2.6e-128;
0; Mismatches 157; Indels
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597 c 650 g 778 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Lu30"
/lab_host="DH10B"
                                                                                                                                                                 /organism="Mus musculus"
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/un.xell="Landon decoration of the follower of the first strand cDNA synthesis was brimer containing a Not I site. Double stranded cDNA was ligated to an Ecot a daptor, dispested with Not I, and cloned directionally into pTTT3-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GCTCAAGGCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                00015321 686 bp mRNA linear BST 26-MAR-2002 II-H-ED1-axw-j-04-0-UI.s1 NCI CGAP_ED1 Homo sapiens cDNA clone :MAGE:5834595 3', mRNA sequence.
                                                                       1219 cerranactracananangraccareneneerecrirenerreneneeneenanaereeneeneeneen 1278
                                                                                                                                                                                                                                               1279 GGATTGCATAAGTCACTCATTGATGTGGCTCTGGAACACCACGAGGAATGTGACTGTGTG 1338
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Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA=Yes.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 686)

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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
AGCAAAGTTACTAAAAAATACCACGAGGTCCTTCAGTTGAGACCAAASACCGGTGTCAGG
                                                                                                                                                                    GGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTG
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Pred. No. 1.7e-117;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159 3 Shibata,K., Itob,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamua,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watamahki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer 20530913 11076861		And Hayashizaki, Y. And Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851 5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (Dases I to 2502) 6 (Dases I to 2502) 7 Analysis of Length cDNAs Nature 420, 563-573 (2002)	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayatsun, M., Hiramoto, K., Hiroka, T., Hirozane, T., Hayashida, K., Hayatsun, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kolima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Numazaki, K., Ohnato, M., Ohaato, N., Okazaki, Y., Salto, R., Saltoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Ohaato, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Takahashi, F., Takaku-Akahira, S., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genome -csegso. riken.go.jp, RIKEN Yokohama Institute; 1-7-2 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegso. riken.go.jp, Raxis H-45-503-9216, Sano,
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Matches 665; Conservative 1; Mismatches 6; Indels 2; Gaps 2; QY 859 CAAASACCGGTGTCA-GGGATTGCACAAATCACTCACCGACGTGGCCTGGAGCACCATG 918 Db 686 CAAAGGTGTCA-GGGATTGCACAAATCACTCACCGACGTGGCCCTGG 628 QY 919 AGGAGTGTGACTGTGTGCAGAGGACACAGGAGGACAATCACCACCACCACCACCACGCAGG 978 Db 627 AGGAGTGTGTGTGTGCAGTGCAGTGCACAGGAGGATTACTATTAGAGAACGTTGTCT 568 QY 979 TCTTGCCCAGAGCTGTGCAGTGCAGTGCTGATTCTATTAGAGAACGTATCTT 508 Db 567 TCTTGCCCAGAGCTGCAGTGCAGTGGTGATTCTATTAGAGAACGTATCTT 508 QY 1039 CATCCTTAATCTCAGTTTTAAAGGAACCTTTCATCTTACAGGATTT	Qy 1099 CTGAAAGAGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGC 1158 Db 447 TTGAAAGAGAGACATCAAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGGGC 388 Qy 1159 CTAAAGGACAGGACAAACAGCTCTCCAATCGTGGAAAGAAA		RESULT 14 AK081347 LOCUS Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30008P20 product:platelet-derived growth factor, C polypeptide, full insert sequence. Max081347 AK081347 AK08134 A

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1. .789
/organism="Homo sapiens"
                                                    816 AGCAAAGTTACTAAAAAATACCACGAGGT
                                                                           968 CGTAAAGTTACAAAAAGTACCATGAGGT
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/db_xref="taxon:9606"
/clone="IMAGE:5214461"
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99.0%; Pred
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                                                                                                                                                                                                                                                                                                                              AACGGAGTACAAGATCCTCAGCATGAGAATTATTACTGTGTGTACTAATGGAAGTATT
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                                                                                                                                                                                                                                                                          39.3%; Score 604.2; DB 11; Length 2502; ilarity 84.2%; Pred. No. 2e-110; Conservative 0; Mismatches 128; Indels 0;
Please visit our web site for further details.
URL:http://ganome.goc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                                                          /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="C130008P20"
                                                                                                                                          /tissue_type="head"
/clone_lib="RIKEN full-length
                                                                                                                                                                 /dev stage="16 days embryo"
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/tissue_trpe="leukcyte"
/lab host="hulbs"
/clone lib="with McC with McC wit
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815
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 789)
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Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov acolumn: 06
High quality sequence start: 26
High quality sequence stop: 762.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Pred. No. 5.3e-104;
); Mismatches 6;
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Db 321 GCAGTAGAGGAAATGTATGGATACATTAGTTTGATGAAGAAGTTTGGGCTTGAAGAC 380

216 CCAGAAGATGACATATGCAAGTATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACT 275

Db 381 CCAGAAGATGACATATGCAAGTTTTGTAGAAGTTGAGGAACCCAGTGATGGAACT 440

Qy 276 ATATTAGGGCCTGGTGTGGTTCTGGTACTGAAGGAAAT 500

A41 ATATTAGGGCCTGGTGTGTTCTGTACTGATACAGGAAACAGATTTCTAAAGGAAAT 500

Qy 336 CAAATTAGGATAAGATTTGTATCTGATACTGTACCAGGAATTTCTAAAGGAAAT 500

Qy 336 CAAATTAGGATAAGATTTGTATCTGATAGTATTTTCTTCTTGAACCAGTTCTGATC 560

Qy 396 CACTACAACATTGTATCTGATGAATATTTTCTTCTTCTGAACCAGTTCTGCATC 560

Qy 396 CACTACAACATTGTATCTGATGAATATTTTCTTCTTCTGAACCAGGTTCTGCATC 560

Qy 456 CACTACAACATTGTATTGTATCACAGAAGTTGAACTGTACTCCTTCAGTGCTCCCCT 620

Qy 561 CACTACAACATTGTCATGATCTAATAATTTTCTTTAGTACTTTGAAGGAAT 680

Qy 576 CTTATTCGATATTTGAACTGTTAATAATGCTATAAAGAAGAC 680

Qy 576 CTTATTCGATATCTTGAACCAGAAGATGAACTTTAGTACTTTAGTACTTGGAAGAC 680

Qy 577 ACTTGCCACTGGACCTGCTTAATAATGCTATAAATGAAGTTATATAAGGCCA 740

Qy 577 ACTTGCCAACAACTTTGTATTGTTTTTGAATAAATGAAATTATTAGAAGATCTTATATAAGGCCA 740

DD 577 ACTTGCCAACAACTTTGTATTGTTTTTGAAAGAAA 782
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Search completed: November 26, 2003, 05:47:49 Job time : 2245.94 secs

VEGF-X

AAB10650 AAB10651 AAB19578

Human 990128vegx p
Human WEGF-X prote
Human PRO200 (vasc
Human PRO213 prote
Human PRO713 prote
Human TANGO 128.
Human growth facto
Amino acid sequenc
Bone morphogenic p
Human zvegf3 polyp
Polypeptide for hu
Human PRO200 polyp
Human WEGF/PDGF-11

AAB33414 AAB24412 AAB01419 AAY96858 AAY84557 AAY556503 AAG65603 AAU08465 Human Zvegf3 prote
Human PRO200 prote
Human PRO200 prote
Human PRO200 prote
Human anglogenesis
Human vacqular end
Human VEGF-1ike pr
Human VEGF/PDGF-1i
Human zvegf3 prote
Human zvegf3 prote

AAB74028 AAE02649 AAE00997

AAB50980

AAB49895 AAB53074 ABB79984

Human prowth facto Human PRO polypept Human secreted/tra Novel secreted and Human PRO200 polyp Human vascular end

ABG92889
ABB81331
ABB81331
AAV76684
AAV76684
AAB776331
ABG76391
ABG6712
ABG6712
ABG6712
ABG76393
ABG76393
ABG76393
ABG76393
ABG7639
AAB10634
AAB10639
AAB10639
AAB10639

1728 1728 1728 1728 1720 1720 1720

Human VEGF-X prote Human VEGF-X homol Human VEGF-X prote Human growth facto Human VEGF-X prote

ALIGNMENTS

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November 25, 2003, 20:55:13; Search time 33.125 Seconds (without alignments) 1523.775 Million cell updates/sec
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| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
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| SIDSI/gcgdata/geneseqfygeneseqp-embl/AA199.DAT:*
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| SIDSI/gcgdata/geneseqfygeneseqp-embl/AA2003.DAT:*
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| SIDSI/gcgdata/geneseqfygeneseqp-embl/AA2003.DAT:*
| SIDSI/gcgdata/geneseqfygeneseqp-embl/AA2003.DAT:*
| SIDSI/gcgdata/geneseqfygeneseqp-embl/AA2003.DAT:*
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                                                                                                                                                                                                                                                                 1734
1 GKEQFSSNKEQNGVQDPQHE.....DVALEHHEECDCVCRGSTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                              1107863
                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                               1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         using sw model
                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length: 0
length: 2000000000
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                                     Copyright
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Maximum DB
                                                                                                           protein
                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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Platelet-derived growth factor C; PDGF-C; cell proliferation, growth factor; heparin; connective tissue; wound healing; VBGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
                                                                   A fragment of platelet-derived growth factor C (PDGF-C).
                                                                                                                                                                                                           /note= "encoded by AAS"
                                                                                                                                                                                  Location/Qualifiers
287
AAY84558 standard, Protein, 318
                                                                                                                                                                                                                                                                                                     98US-0102461.
98US-0108109.
98US-0110749.
98US-0113002.
                                                                                                                                                                                                                                                                                 99WO-US22668
                                            (first entry)
                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                   WO200018212-A2
                                                                                                                                                                                                                                                                                                      30-SEP-1998;
12-NOV-1998;
03-DEC-1998;
18-DEC-1998;
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                 30-SEP-1999;
                                            25-JUL-2000
                                                                                                                                                                                                                                                          06-APR-2000
                      AAY84558;
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A fragment of plat Human VBGF-B prote Human PRO210 prote Human vascular end Human zvegf3, SEQ Human platelet-der Human PRO200 (UNQ1 Human RACE generat Human VEGF-X prote

> AAY33679 AAY41766 AAY30023 AAB48657 AAB24250 AAB10633 AAB10633

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AAY84558

В

Length

Query Match

Result No.

Description

11-JAN-2000 (first entry)

AAY33679;

Human VEGF-E

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The present sequence represents a human platelet-derived growth factor C (PDGF-C) (formally designated VBGF-F) fragment. PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of calls expressing a PDGF-C receptor. PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour proper continuous and erythroleukemia, can be identified by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue remodaling during invasion of tumour calls into a normal population of cells. Antagonists can also be used to inhibit tissue
                                                                                                                                                                                                                                      Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C
                                                                                                                     Uutela M, Alitalo K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially found in the lung, kidney or liver.
                                                                                                                 Lee X, Ponten A,
Betsholz C;
                                                                            UNIV HELSINKI LICENSING LTD
                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 135pp; English.
                                                         LUDWIG INST CANCER RES
                   99US-0144022.
                                                                                                                     Aase K,
Heldin C,
                                                                                                                                                                                 WPI; 2000-292954/25
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                   15-JUL-1999;
                                                                                                                     Eriksson U,
                                                                                                                                        Oestman A,
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240 LIFDERFGLEDPEDDICKYDFVEVEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120 LIFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDV 300 1 GKFQFSSNKEQNGVQDPQHERIIIVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQ 60 1 GKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQ EYPPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPER WQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTD ö Length 318; Indels 100.0%; Score 1734; DB 21; 100.0%; Pred. No. 7.6e-167; 0; Mismatches ALEHHEECDCVCRGSTGG 318 ALEHHERCDCVCRGSTGG 318 Best Local Similarity 100. Matches 318; Conservative 61 61 121 181 241 241 Query Match 121 181 301 301 QΩ a 셤 셤 g ò ਨੇ ò à ð

61 88

KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL

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AAY33679 standard; Protein; 345 AA.

AAY33679 ID AAY3 RESULT 2

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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially by manners in mammals, especially by the used to treat described hypertrophy content or useful in wound repair and tissue generation and may especially be used to treat described hypertrophy content or manners and administered to treat dadministered to treat administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or soreen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or cardiovascular, endothelial or angiogenic disorders in mammals (especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (especially to diagnose or articody-VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in them ammals, by detecting abnormally high or low VEGF-E gene expression in cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cample. They may also be used to produce probes useful to detect related to a protein described in the method of the invention.
                                                                                                                                                   VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.
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100.0%; Pred. No. 3.4e-166;
ive 0; Mismatches 0;
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Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC.
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                              YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181
                                                                                                                                                                                                                 Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
                                                        YFPSEPGFCIHYNIWMQFTEAVSPSVLPPSALPLDLLMNAITAFSTLEDLIRYLEPERW
     TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE
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                                                                                                              LEHHEECDCVCRGSTGG 318
                                                                                                                    Human PRO200 protein sequence.
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98US-0079663.
98US-0079664.
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12-WAR-1998;

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27-WAR-1998;

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21-WAR-1998;

31-WAR-1998;

31-WAR-1998;
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08-APR-1998;
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      (GETH ) GENENTECH INC.
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N-PSDB; AAZ34296.
08-APR-1998

08-APR-1998

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22-MAY-1998
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<u>ب</u> Chen

New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -

Claim 12; Fig 207; 530pp; English.

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WPI; 1999-458680/38.
N-PSDB; AAX86352.
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                                                                                                                                                                                                                                                                                                                                                                                              88
The present invention describes secreted and transmembrane polypeptides and their polymucleotides. The mucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to traet a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. Apa3891 to AAZ34338, and AAY41685 to AAY41774 represent polymucleotide and polypeptide sequence given in the exemplification of the present
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tissue growth inhibition; tumour growth; cancer; tissue growth;
angiogenesis; coronary artery blockage.
                                                                                                                                                                                                                                                                       99.7%; Score 1728; DB 20; Length 345; 100.0%; Pred. No. 3.4e-166; ive 0; Mismatches 0; Indels 0.
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98US-0072635.
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Matches 317; Conserv
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                                                                                                                                                                                                    related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that antagonize its activity. VEGF-R antagonize its activity. VEGF-R antagonists (e.g. anti-VEGF-R antibodies) are useful for inhibiting transcriber. This is useful for inhibiting tumour growth and for treating cancer. VEGF-R itself can be used to stimulate tissue growth, anglogenesis and to treat coronary artery blockage. The VEGF-R coding sequence can be used for the recombinant production of the VEGF-R protein.
                                                                                                                                                                           growth factor
growth factor related protein and related for identifying antagonists and binding
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                                                                                                                                                                              The present sequence represents a vascular endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.7%; Score 1728; DB 20;
100.0%; Pred. No. 3.4e-166;
ive 0; Mismatches 0;
                                                                                                                  Claim 1; Page 56-58; 62pp; English.
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A vascular endothelial
polynucleotide, useful
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Matches 317; Conserv
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269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 328
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                                                                LEHHEECDCVCRGSTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acids; the recombinant expression of human zvegf4; an antibody which binds to human zvegf4 or a fragment thereof; a method of activating which binds to human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a method of modulating the proliferation, differentiation, migration or metabolism of bone cells, comprising exposing bone cells to zvegf4-derived polypeptides; and a method of detecting a genetic abnormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived cannormality in the zvegf4 gene of a patient. Zvegf4 proteins and derived callular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to modulate neurite growth (e.g., in the treatment of Alzheimer's disease or multiple sclerosis). Due to their osteogenic activity, they may also be used in the treatment of periodontal disease and fractures. They may also be used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member of the PDGF (platelet-derived growth factor)/USGF (vascular endothelial growth factor) family. Zvegf4 has a growth factor domain (ABA88654) characterised by a PDGF cystine knot structure, and a CUB domain chas abeta barel structure. Zvegf4 has a PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 tusions; expression constructs and host cells comprising human zvegf4.
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                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to the human growth factor homologue
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                                                                                                                                                                                        Sheppard PO,
                                                           03-MAY-1999; 99US-0304216.
10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
                        03-MAY-2000; 2000WO-US40047.
                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
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Matches 317; Conservative
                                                                                                                                                                                          Hart CE,
                                                                                                                                                                                                                                    2000-687541/67.
                                                                                                                                                                                                                                                                                                                                               Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                              Human, platelet derived growth factor related protein, LP8, VEGFh, vascular endothelial growth factor h, tissue regeneration, vulnerary, atherosclerosis, PDGF-related protein, antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist
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                                                                                                                                                                                                                                                                            Human platelet-derived growth factor related protein LP8.
AAB24250 standard; Protein; 345 AA.
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I FWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 328
activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bicactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bicactive molecules to cells. AAC78600 to AAC7897 represent FCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA
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                                                                                                                                                                                                                                                                                                                                                         149 YFPSERGKCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW
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                                                                                                                                                                Length 345;
                                                                                                                                                                                            Indels
                                                                                                                                                               99.7%; Score 1728; DB 21;
100.0%; Pred. No. 3.4e-166;
ive 0; Mismatches 0;
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99US-0124967.
99US-0164131.
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nes 317; Conservative
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Xu J;
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                                                                                                                                     345 AA;
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18-MAR-1999;
08-NOV-1999;
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                          QLDLEDLYRPTWQLLGKAFVPGRKSRVVDLNLTTEEVRLYSCTPRNFSVSIREELKRTDT 268
                                                                            QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT 241
                                                             IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC78458 to AAC78599 represent polynucleotide and BST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polynucleotides and polypeptides have cytostatic
                                                                                                                                                                                                                                                                                                                                      Human, secreted protein, transmembrane protein, PRO; EST; cytostatic, expressed sequence tag; detection; cancer.
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                                                                                                                                                                                                                                                                                                            Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
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                                                                                                                                                                                                                         AAB44322 standard; Protein; 345
                                                                                                                     LEHHEECDCVCRGSTGG 318
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12-APR-1999; 99US-01131445.
13-AUX-1999; 99US-01131445.
23-AUX-1999; 99US-0145698.
25-AUX-1999; 99US-0145698.
20-NOV-1999; 99US-0162506.
30-NOV-1999; 99WO-US28551.
02-DEC-1999; 99WO-US28551.
30-DEC-1999; 99WO-US31243.
30-DEC-1999; 99WO-US31244.
30-DEC-1999; 99WO-US31244.
30-DEC-1999; 99WO-US31274.
30-DEC-1999; 99WO-US31274.
30-DEC-1999; 99WO-US31274.
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9903-0126773.
9903-0130232.
9903-0134287.
9903-0141037.
9903-014037.
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Filvaroff E,
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N-PSDB; AAC78582.
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Goddard A, (
Kljavin IJ,
Shelton DL,
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29-MAR-1999;
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                                                                                                                             This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antithematic, antiantitic, antiporiatic and auticabetic activity and acts as a nangiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating corer, rheumatoid archritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the RACE generated human VEGF-X protein described in the method of the invention.
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                                                  New vascular endothelial growth factor protein, useful for treating or
preventing diseases associated with inappropriate angiogenesis activity
such as cancer, rheumatoid arthritis, psoriasis and wounds -
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100.0%; Pred. No. 3.4e-166;
ive 0; Mismatches 0;
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            2000-442669/38
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                 345 AA;
                                                                                                        Disclosure, Fig
                          N-PSDB; AAA71951
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, ortostatic, antitheumatic, antibacinatic and acts as a nangiogenesis and vascularization antidiabetic activity and acts as a nangiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration. This sequence represents the human VEGF-X protein isolated from clones 4 and 7 described in the method of the invention.
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100.0%; Pred. No. 3.4e-166;
iive 0; Mismatches 0;
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graft
venous sore; diabetic ulcer; burns; skin
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                                                                                                                             WO200037641-A2
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Dhanaraj SN,
                                                                Homo sapiens
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242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA

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TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE

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This invention describes a novel vascular endothelial growth factor-X (VBGF-X) protein (1a) and its encoding polynucleotide (11a) which has vulnerary, cytostatic, antirheumatic, antiantitic, antipsoriatic and antialabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid archritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue regarding medicaments for treating wounds such as dermal ulcers, preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents a human VEGF-X protein
                                                                                                                                                                                                                        VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogeneeis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dijkmans JJH, Gosiewska A;
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                                                                                   AAB10644 standard; Protein; 345
LEHHEECDCVCRGSTGG 345
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                                                                                                                                                                                         Human VEGF-X protein #4.
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N-PSDB; AAA71990.
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This invention describes a novel vascular endothelial growth factor.X (VBGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnezary, cytostatic, antirheumatic, antiarchritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retlinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful
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                                                                                                                                                                                  YPPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW
                                                        QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT
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                                                                                                                                                                                                                                                                                                                                       AAB10650 standard; Protein; 345
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Xu J;
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08-NOV-1999;
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for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair; proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity o vascularization. This sequence represents the human 990126vegx protein used to illustrate the method of the invention.
                                                                                                                                                                                                         29 KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL
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                                                                                                                          99.7%; Score 1728; DB 21; 100.0%; Pred. No. 3.4e-166;
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Matches 317; Conservative
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Xu J;
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polymucleotide (IIa) which has vulnezary, ortostatic, antiphermatic, antiparitation, antiporitatic and antidabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating correct theumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein
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                New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
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Pred. No. 3.4e-166;
0; Mismatches 0;
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100.0%; Pri
                                                                                                 72; Fig 12; 127pp; English
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Best Local Similarity 100.
Matches 317; Conservative
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The present sequence is that of human PRO200 or vascular endothelial growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88519) that was isolated from a glioma cell line G61 library using probes (see AAA8852-26) based on an expressed sequence tag (see AAA88522) that showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a pl of about 6.06. A method for producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay, prevent or rescue retinal ganglion cells, displaced retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal ganglion cells, macrine cells, displaced anacrine cells, displaced anacrine cells, including wheller cells and cells, and supportive cells (including Mueller cells and cells are preferably photoreceptors and photoreceptor cells indivity or by an ocular disease selected from retinitis pigmentosa, macular cells in a caused by retinal injury, light or environmental trauma or by an ocular disease selected from retinial detachment, retinal cells, macular holes, cells are myopia, acute retinal necrosis syndrome, traumatic cells charm, celinopathy, retinal diseases, thrombocytopenic purpura, cellusion, collagen vascular diseases, thrombocytopenic purpura, cocclusion, retinal vasculltis and occlusion associated with Eales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel PRO polypeptides useful for preventing or rescuing retinal cells from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia, uveitis -
                                                                                                                      note≈ "Asn is N-glycosylated"
                                                                                                                                                     "Asn is N-glycosylated"
                                                                                                                                                                                   note≈ "Asn is N-glycosylated"
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282..288
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319..325
/note= "Amidation"
                                                                                                                                                                                                                                                                              "N-myristoylation"
                                                                                                                                                                                                                 "N-myristoylation'
                                                                                                                                                                                                                                                "N-myristoylation"
                                                          'label= Signal peptide
                                                                         15..345
/label= Mature_Pro200
                             Location/Qualifiers
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Kuo SS, L
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Kljavin IJ,
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N-PSDB; AAA88515.
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   Homo sapiens
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Klein RD,
                                                                          Protein
                                          Peptide
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Henzel WJ, Kabakoff RC; Wood WI;

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Human; immune related disease; diagnosis; antiinflammatory; cardiant;

dermatological; antiathritic; antitheumatic; immunosuppressive;

haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;

matiansemic; hepatotropic; virudide; antipsoriatic; antiallergic;

antiathmatic; systemic lugus erythematosus; rheumatoid arthritis;

misschmatic; systemic pathy; systemic sclerosis; thyroiditis;

widiopathic inflammatory myopathy; systemic sclerosis; sarcoidosis;

widiopathic inflammatory myopathy; systemic sclerosis; sarcoidosis;

wattoimmune thrombocytopaenia; immune-mediated renal disease;

autoimmune disease; hepatobiliary disease; Milpple's disease;

mitchmuned disease; immune-mediated skin disease;

mutoimmune disease; immune-mediated skin disease;

munuological disease; irmnaplantation associated disease;

munuological gasett-versus-host-disease.
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                                                                                                                                                                                                  0; Indels
disease and systemic lupus erythematosus (claimed).
                                                                                                                               99.7%; Score 1728; DB 21;
100.0%; Pred. No. 3.4e-166;
ive 0; Mismatches 0;
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99US-0128849.
99WO-US08615.
99US-0131445.
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Matches 317; Conservative
                                                                      345 AA;
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10-MAR-1999;
12-MAR-1999;
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12-APR-1999;
20-APR-1999;
28-APR-1999;
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                                                                      Sequence
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Gurney AL, Hebert C, Henzel W; ), Shelton DL, Smith V; rood WI, Yan M;
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in J, Pennica D, Shelto
Watanabe CK, Wood WI,
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              99WO-US12252
99US-0141037.
99US-0145698.
99US-0145698.
99US-0146222.
99WO-US20111.
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99WO-US28564.
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Kabakoff RC, Lu Y, Pan J,
Stewart TA, Tumas D, Watan
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2000WO-US00376.
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99WO-US28634
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2000WO-US04341.
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02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
05-JAN-2000;
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18-FEB-2000;
18-FEB-2000;
04-MAY-1999,
14-MAX-1999,
02-UM-1999,
23-UM-1999,
26-UM-1999,
28-UM-1999,
08-SEP-1999,
01-SEP-1999,
115-SEP-1999,
15-SEP-1999,
15-SEP-1999,
15-SEP-1999,
05-OCT-1999,
05-OCT-1999,
05-OCT-1999,
05-OCT-1999,
05-OCT-1999,
05-OCT-1999,
05-OCT-1999,
05-OCT-1999,
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                                                                                                                            30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
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Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, costeoathritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroidits, diabetes mellitus, immune-mediated renal disease, diseases, cluten-sensitive enteropathy and Whitpple's disease, and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel diseases, gluten-sensitive enteropathy and Whitpple's disease, autoimmune or immune-mediated skin diseases, allergic diseases, cuttoimmune or immune-mediated skin diseases, allergic diseases, controlading graft rejection and graft-versus-host-disease.

CC diseases including graft rejection and graft-versus-host-disease.

AAC58397 to AAC58978 represent PCR primers and hybridisation probe used in the isolation of human PRO sequences. AAC58397 to AAC58972 controlation and protein c sequences given in the exemplification of the present invention.

345 AA; Sequence

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Query Match 99.7%; Score 1728; DB 21; Length 345; Best Local Similarity 100.0%; Pred. No. 3.4e-166; Matches 317; Conservative 0; Mismatches 0; Indels 0
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Paoni NF, Smith V;
           29 KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL
                                                    149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW
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                                          TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE
                                                                                    YPPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW
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 KPQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVMRLVAVEENVWIQL
                                                                                                                               QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT
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Gurney AL, Klein RD,
Williams PM, Wood WI;
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Godowski PJ,
Watanabe CK,
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NY WPI; 2000-412154/35.

N W-PSDB; AAA77621.

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Nucleic acids encoding PRO polypeptides useful for preventing,
PT Aucleic acids encoding diagnosing a cardiovascular, endothelial or
Anglogenic disorders in mammals -

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Claim 72; Fig 50; 315pp; English.

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CThe present invention describes nucleic acids encoding PRO polypeptides
CC ardiovascular, endothelial or angiogenesis and cardiovascularist endothelial or angiogenic disorder in mammals by
CC modulating cell profileration, angiogenesis and cardiovascularisation,
and for identifying agonists and antagonists of these processes. The
CC modulating cell profileration, angiogenesis as associated with
CC motelic acids and the proteins they encode may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC prevention, treatment and diagnosis of diseases associated with
CC angiogenic disorders in mammals (e.g. atherosclerosis, cancers and
CC cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors
CC containing them and the PRO polypeptide may be used to treat disorders
CC AAB24388 to AAB24435 represent nucleotide and protein sequences used in
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Sequence 345 AA;

Sequence 345 AA;
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ö TFDERFGLEDPEDDICKYDFVEVEEFSDGTILGRWCGSGTVFGKQISKGNQIRIRFVSDE 148 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181 QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIRELKRTDT 241 149 YFPSEPGFCHYNIVMPQFTEAVSPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERW 208 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121 2 KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL 61 29 KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWARLVAVEENVWIQL 88 99.7%; Score 1728; DB 21; Length 345; 100.0%; Pred. No. 3.4e-166; tive 0; Mismatches 0; Indels 0; LEHHEECDCVCRGSTGG 318 LEHHEECDCVCRGSTGG 345 Best Local Similarity 100. Matches 317; Conservative 62 89 122 182 209 302 Query Match g g g à gg ò ò qq ò

Search completed: November 25, 2003, 21:02:14 Job time : 34.125 secs us-09-852-209a-5.rai

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Sequence 2, Ap
Sequence 18, A
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1734
1 GKRQFSSNKEQNGVQDPQHE......DVALEHHEECDCVCRGSTGG 318
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-540-224-5
US-09-540-55-66-3
US-09-56-66-43
US-09-564-595D-35
US-09-564-595D-55
US-09-564-595D-57
US-09-564-595D-53
US-09-564-595D-53
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922 4 US-09-116-473-4 926 3 US-08-936-135-20 101 3 US-09-374-135-6 925 4 US-09-116-473-2 901 3 US-08-936-133-26 906 3 US-08-936-135-24 906 3 US-08-936-135-24 909 3 US-08-936-135-14 914 3 US-08-936-135-14 916 3 US-08-936-135-14 917 4 US-09-936-135-14 918 4 US-08-936-135-14 918 4 US-08-936-135-14 918 4 US-08-936-135-14 918 5 US-08-936-135-14 918 5 US-08-936-048A-4 949 2 US-08-839-008-9 9415 3 US-08-939-008-9	ALIGNMENT)9040220D)ne OLYPEPTIDES HAV IN 1 AND NUCLEIC ROCESSES FOR THE : US/09/040,220D	# Score 1728; DB 4; Pred. No. 2.1e-17 Mismatches
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                                                                             APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Diddington, Christopher S.
APPLICANT: Shoepard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilberteer, Kimberly E.
APPLICANT: Gilberteen, Debra G.
TITLE OF INVENTION GROWTH FACTOR HOMOLOG ZVEGF9
FILE REFERENCE: 1996-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
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Fatent No. 6455283
GENERAL INFORMATION:
FAPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO
FILE REFERENCE: P112222
CURRENT APPLICATION NUMBER: US/09/265,686
CURRENT FILING DATE: 1999-03-10
FRIOR APPLICATION NUMBER: US 09/040,220
FRIOR APPLICATION NUMBER: US 09/184,216
FRIOR APPLICATION NUMBER: US 09/184,216
                              ; Sequence 2, Application US/09457066; Patent No. 6432673; GENERAL INFORMATION:
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Matches 317; Conservative
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TYPE: PRT
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Sequence 5, Application US/09540224
| Sequence 5, Application US/09540224
| Patent No. 6466543
| GENERAL INFORMATION:
| APPLICANT: Gilbertson, Debra G. | APPLICANT: Gilbertson, Debra G. | TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
| TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
| FILE REFERENCE: 00-28
| CURRENT FILING DATE: 2000-03-31
| EARLIER APPLICATION NUMBER: US 60/180,169
| BARLIER FILING DATE: 2000-02-04
| NUMBER OF SEQ ID NOS: 9
| SOFTWARE: PastSEQ for Windows Version 3.0
| SEQ ID NO 5
                                                      Indels
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99.7%; Score 1728; DB 4; L
100.0%; Pred. No. 2.1e-179;
.ive 0; Mismatches 0;
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99.7%; Score 1728; DB 4; L
Best Local Similarity 100.0%; Pred. No. 2.1e-179;
Matches 317; Conservative 0; Mismatches 0;
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Query Match 99.7
Best Local Similarity 100.
Matches 317; Conservative
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US-09-540-224-5
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29 KRQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFFPHTYPRNTVLVWRLVAVEENVWIQL
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; Sequence 43, Application US/09457066
; Patent No. 6412673;
; GENERAL INFORMATION:
    APPLICANT: Gao, Zeren
; APPLICANT: Brepard, Paul O.
    APPLICANT: Sheppard, Paul O.
    APPLICANT: Shepmard, Paul O.
    APPLICANT: Shepmard, Paul O.
    APPLICANT: Shepmard, Paul O.
    APPLICANT: Shepmard, Paul O.
    APPLICANT: Gilbertson, Debra G.
    APPLICANT: Gilbertson, Debra G.
    APPLICANT: West, James W.
    TITLE OP INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
    FILE REFERENCE: 98-60
    CURRENT APPLICATION NUMBER: US/09/457,066
    CURRENT PILING DATE: 1999-12-07
    NUMBER OF SEQ ID NOS: 50
    SOPTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 43
    ITNPE: PRT
                    APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706, 968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-33.1
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
Shoemaker, Kimberly E.
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Best Local Similarity 100.
Matches 317; Conservative
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US-09-457-066-43
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242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
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                                                                                                                                                                                                                                                                                       APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 1999-05-03
PRIOR PILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR PLILING DATE: 1999-11-10
PRIOR PLILING DATE: 1999-05-03
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 345
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APPLICANT: Gao, Zeren; APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
                                                                                                                                                                                        RESULT 5
US-09-564-595D-33
US-09-564-595D-33
Sequence 33, Application US/09564595D
Patent No. 6495668
GENERAL INFORMATION:
                                                                                    LEHHEECDCVCRGSTGG 318
                                                                                                                      329 LEHHEECDCVCRGSTGG 345
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Best Local Similarity 100.
Matches 317; Conservative
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ORGANISM: Homo sapiens
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US-09-706-968-2
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                          209 QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT
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Best Local Similarity 87.1<sup>1</sup>
Matches 276; Conservative
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269 IFWPGCLLVKRCGGNCACCLANCNECQCVPRKVTKKYHEVLQLRPKTGVKGLHKSLTDVA 328
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; Batent No. 6528050
; GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Gao, Zeren
APPLICANT: Piddington, Christopher S.
APPLICANT: Bidepard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gliberteon, Debra G.
APPLICANT: Gliberteon, Debra G.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Number G.
CURRENT FRERENCE: 98-6C01
FILLE REFERENCE: 98-6C01
CURRENT FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FRAESEQ for Windows Version 3.0
SEGURATION OF ASPLICANT ON ATTENTION OF SEQ ID NOS: 50
SOFTWARE: FRAESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.9%; Score 1559; DB 4; Best Local Similarity 87.1%; Pred. No. 4.9e-161; Matches 276; Conservative 26; Mismatches 15;
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Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF4
FILE REFERENCE: 99-19
                                                                                                                                         329 LEHHEECDCVCRGNAGG 345
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                                                                                  LEHHEECDCVCRGSTGG
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US-09-706-968-43
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                                                            KLOLSSDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQL 88
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                                  KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVMRLVAVEENVWIQL
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Sequence 35, Application US/09564595D

Setent No. 6495668

GENERAL INFORMATION:
APPLICANT Gilbert, Teresa

APPLICANT Hart, Charles E.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4

FILE REFERENCE: 99-19

CURRENT FILING DATE: 2000-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR APPLICATION NUMBER: US 60/180,169

PRIOR FILING DATE: 1999-05-04

PRIOR FILING DATE: 1999-05-04

SPRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

SPRIOR FILING DATE: 1999-05-04

SPRIOR FILING DATE: 1999-05-04

SPRIOR FILING DATE: 1999-05-04

SPRIOR FILING DATE: 1999-05-04

SPRIOR FILING DATE: 1999-05-05

PRIOR FILING DATE: 1999-05-04

SPRIOR FILING DATE: 1999-05-05

SPRIOR FILING DATE: 1990-05-05

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89.9%; Score 1559; DB 4;
Best Local Similarity 87.1%; Pred. No. 4.9e-161;
Matches 276; Conservative 26; Mismatches 15;
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CRGANISM: Mus musculus
US-09-564-595D-35
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US-09-564~595D-35
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                                                                           29 KLQLSSDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNWVLVWRLVAVDENVRIQL
                                                                                                                                           62 TFDERFGLEDPEDDICKYDFVEVEBPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE
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                                             2 KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL
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80 DFVEVEREPSDGT -- ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVM 137
                                                                                                                                                                       61 DFVEVEDDISETSTIIRGRWCGHKEVPPRIKSRINQIKITFKSDDYFVAKPGFKIYYSL-L 119
                                                                                                                                                                                                                                                           120 EDFQPAAASVSPSVLPPSALPLDLIANAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWO 179
                                                                                                                                                                                                                                                                                                                        195 LLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCG 254
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                                                                               2 DETIQVKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDICKX
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                                                     20 ERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKY
             Gaps
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           33; Indels
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APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Gheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT FILING DATE: 2000-05-03
FRIOR PILING DATE: 1999-05-03
FRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 2000-02-04
NUMBER: OF SEQ ID NOS: 57
NUMBER: OF SEQ ID NOS: 57
SEQ ID NO S: 57
LENGTH: 316
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67.1%; Pred. No. 5.7e-111;
ilve 26; Mismatches 55;
           24; Mismatches
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; Patent No. 6495668
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Matches 210; Conservative
           240; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIRELKRTDTIFWPGCLLVKRCGGNCA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 HERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.4%; Score 1325; DB 4; Length 3 Best Local Similarity 82.8%; Pred. No. 1.1e-135; Matches 246; Conservative 14; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOS-US-US-US-LS)

Sequence 57, Application US/09564595D

Sequence 57, Application US/09564595D

GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa

APPLICANT: Gilbert, Teresa

APPLICANT: BAEPERG, Paul O.
TITLE OF INVENTION: GROWTH PACTOR HOMOLOG ZVEGF4

FILE REPERENCE: 99-19

CURRENT APPLICATION NUMBER: US/09/564,595D

CURRENT FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-05-03

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1999-11-10

PRIOR FILING DATE: 1909-11-10

SEGING SEGINO NUMBER: US 60/180,169

PRIOR FILING DATE: 1900-02-04

SOFTWARE: FastSEQ for Windows Version 4.0

SEGIND NO 57
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Pred. No. 2.6e-129;
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASLSEQ for Windows Version 4.0
SSOFTWARE: FASLSEQ for Windows Version 4.0
ENGTH: 302
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US-09-564-595D-57
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ORGANISM: Artificial Sequence
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78.9%;
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ORGANISM: Artificial Sequence
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Best Local Similarity
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US-09-564-595D-57
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US-09-540-224-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIRBELKR 238
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                                FWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTD 299
                                                     FFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTMALVD 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLT 297
EDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREELKLANVV 237
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                                                                                                                                                                                                                                                                 APPLICANT: Glibert, Teresa
TITLE OF INVENTION: GWOWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR PPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR PLING DATE: 2000-02-04
NUMBER OF SEC ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
60.6%; Score 1051.5; DB 4
Best Local Similarity 63.8%; Pred. No. 6.5e-106;
Matches 204; Conservative 36; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: fusion polypeptide US-09-564-595D-56
                                                                                                                                                                                                                Sequence 56, Application US/09564595D Patent No. 6495668 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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298 IQLDHHERCDCIC 310
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Sequence 37, Application US/09457066 Patent No. 6432673 GENERAL INFORMATION:

US-09-457-066-37

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 FSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP- 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.7%; Score 741; DB 4; Length 370; Best Local Similarity 46.6%; Pred. No. 4.7e-72; Matches 153; Conservative 52; Mismatches 93; Indels
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Patent No. 6468543

GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224

CURRENT FILING DATE: 2000-03-31

EARLIER FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 370
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Raul O.
APPLICANT: Shoemaker, Rimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 37
LENGTH: 370
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Best Local Similarity 46.6
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-457-066-37
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US-09-540-224-2
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TLEDLIRYLEPERWOLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRN 227
                                                                                    287 --KTGVRGLHKSLTDVALEHHEECDCVC 312
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Search completed: November 25, 2003, 21:06:21 Job time : 12.9881 secs

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November 25, 2003, 21:04:39; Search time 22.3988 Seconds (without alignments) 2618.575 Million cell updates/sec
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1734
I GKFQFSSNKEQNGVQDPQHE.....DVALEHHEECDCVGRGSTGG 318
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT MRW PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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15: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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ion	Sequence 5, Appli equence 2, Appli equence 1, Appli equence 1, Appli equence 149, Appli Sequence 488, App Sequence 488, App Sequence 488, App Sequence 488, App Sequence 488, App Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli
Description	Sequence 1, Sequence 2, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 4, Sequence 4, Sequence 4, Sequence 6, Sequen
SUMMARIES	US-09-882-2004-5 US-09-882-2033-2 US-09-882-3033-2 US-09-818-943-1 US-09-923-995-4 US-09-795-006A-149 US-09-798-203A-488 US-09-978-597-488 US-09-978-192A-488 US-09-99-832A-488 US-09-99-832A-488 US-09-99-832A-488 US-09-978-198-488 US-09-978-198-488 US-09-978-189-488 US-09-978-675-6 US-09-978-688-488
DB	100 100 100 100 100 111 111
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% Query Match	
Score	7 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
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US-09-852-209A-5

Sequence 5, Application US/09852209A

Sequence 5, Application US/09852209A

Sequence 5, Application US/09852209A

GENERAL INFORMATION:

APPLICANT: ERIKSSON, Ulf

APPLICANT: LEE, Xuri

APPLICANT: UUTELA, Marko

APPLICANTON NUMBER: US/09/852,209A

FRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR FILING DATE: 1999-05-21

PRIOR PLICATION NUMBER: 60/113,002

PRIOR PLICATION NUMBER: 60/113,002

PRIOR PLICATION NUMBER: 60/113,002

PRIOR PLICATION NUMBER: 60/113,426

PRIOR PLICATION NUMBER: 60/113,002

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100.0%; Score 1734; DB 10; Length 318;

Query Match

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LENGTH: 345
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                    0; Indels
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APPLICANT: HELDIN, CALTHOUIN,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREPOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Erikesson et al-1064-44740
CURRENT APPLICATION NUMBER: US/00/131,600
CURRENT APPLICATION NUMBER: US/09/410,349
PRIOR APPLICATION NUMBER: US/09/410,349
PRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR PILING DATE: 1998-12-18
PRIOR PILING DATE: 1998-12-18
PRIOR PILING DATE: 1998-12-18
PRIOR PILING DATE: 1998-12-18
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET: 2.0
100.0%; Pred. No. 1.2e-166; ative 0; Mismatches 0;
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; Publication No. US20030092670AI
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, UIF
; APPLICANT: LEE, Karin
; APPLICANT: PONTEN, Annica
; APPLICANT: PONTEN, Annica
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OESTMAN, Arne
HELDIN, Carl-Henrik
    Best Local Similarity 100.0
Matches 318; Conservative
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US-10-131-600-5
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                                                                                                    61 LIFDERFGLEDFEDDICKYDFVEVERFSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
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1 GKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVBENVWIQ 60
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Fatent No. US20020004225A1
GENERAL INFORMATION:
APPLICANT: Hart. Charles B.
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT PAPLICATION NUMBER: 2001-03-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTESEQ for Windows Version 3.0
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RESULT 4

1 GKFQPSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYFRNTVLVWRLVAVEBNVM1Q 60

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89 TFDERFGLEDPEDDICKYDFVEVEREPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148
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; Patent No. US20102151680A1
; GENERAL INFORMATION:
APPLICANT: Alitalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
; TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROTEINS
; TURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT APPLICATION NUMBER: US 60/205,331
; PRIOR PILING DATE: 2000-05-18
; PRIOR PILING DATE: 2000-05-18
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SCFTWARER PATENTIN VET: 2.0
; SEQ ID NO 149
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Query Match
99.7%; Score 1728; DB 9; I
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 5.3e-166;
tive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 317; Conservative
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US-09-795-006A-149
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US-09-795-006A-149
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Fatent No. US20020081700A1
GENERAL INFORMATION:
FALLE REPERENTION:
FILLE REFERENCE: 00-47
CURRENT FILING DATE: 2001-08-07
CURRENT FILING DATE: 2001-08-07
FILOR PILING DATE: 2000-08-07
FRIOR APPLICATION NUMBER: US 60/223,164
FRIOR FILING DATE: 2000-08-07
NUMBER OF ERQ ID NOS: 7
SOFTWARE: FASELSQ for Windows Version 3.0
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100.0%; Pred. No. 5.3e-166;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 317; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 1
LENGTH: 345
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US-09-923-995-4
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PRIOR FILING DATE: 1998-03-29
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079656
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-31
PRIOR PELING DATE: 1998-04-01
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-
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PRIOR APPLICATION UNMER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR PILING DATE: 1998-04-22
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R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082796
R FILING DATE: 1998-04-23
R APPLICATION NUMBER: 60/08336
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stelton, David L.
APPLICANT: Stelton, David L.
APPLICANT: Stelton, David L.
APPLICANT: Stelton, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2630PICII US/09/978,295A
CURRENT APPLICATION NUMBER: 09/91855
PRIOR APPLICATION NUMBER: 09/91855
PRIOR PLIING DATE: 2001-07-3
PRIOR FILING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1998-03-10
PRIOR PRILING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-11
PRIOR PLING DATE: 1998-03-12
PRIOR PLING DATE: 1998-03-12
PRIOR FILING DATE: 1998-03-13
PRIOR PRILING DATE: 1998-03-20
269 IFWPGCLLVKRCGGNCACCLANCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 328
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                                                                                                                                                       Sequence 488, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                           302 LEHHEECDCVCRGSTGG 318
                                                                                                                               329 LEHHEECDCVCRGSTGG 345
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferrara, Napoleon
Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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APPLICANT:
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APPLICANT:
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     62 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: ERIKSSON, U1f
APPLICANT: BRIKSSON, U1f
APPLICANT: BRIKSSON, U1f
APPLICANT: AASE, Karin
APPLICANT: ALSE, Xurin
APPLICANT: DENTEN, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: BISTANA, Arne
APPLICANT: BLIDIN, Carl-Henrik
APPLICANT: BETSHOLIZ, Christer
TILLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, INTILE OF INVENTION WUMBER: U9/10/9/852, 209A
CURRENT FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-12-03
PRIOR PELICATION NUMBER: 60/113, 002
PRIOR APPLICATION NUMBER: 60/113, 02
PRIOR PELING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VOY: 2.0
SECTUANAR:
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Best Local Similarity 100.
Matches 317; Conservative
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-39
PRIOR PLING DATE: 1998-05-05
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08463
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08463
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08463
PRIOR PLING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-13
PRIOR PLING DATE: 1998-05-15
PRIOR PRIOR DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085539
PRIOR PLING DATE: 1998-05-15
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Best Local Similarity 100.
Matches 317; Conservative
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PRIOR APPLICATION NUMBER: 60/07836
PRIOR APPLICATION NUMBER: 60/07836
PRIOR FILING DATE: 1998-03-20
PRIOR PLILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR PRILING DATE: 1998-03-26
PRIOR PLILING DATE: 1998-03-27
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PRIOR PRILING DATE: 1998-03-37
PRIOR PRILING DATE: 1998-03-31
PRIOR PRILING DATE: 1998-03-31
PRIOR PRILING DATE: 1998-03-31
PRIOR PRILING DATE: 1998-04-01
PRIOR PLILING DATE: 1998-04-01
PRIOR PRILING DATE: 1998-04-01
APPLICATION NUMBER: 60/078886
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APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION NUMBER: US/09/978,697
CURRENT APPLICATION NUMBER: 00/062260
PRIOR FILING DATE: 1997-11-03
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-03-11
                                                              209 QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRIDT 268
                                                                                                                                                                         QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT 241
                                                                                                                                       242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Patent No. US20020169284A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                   302 LEHHEECDCVCRGSTGG 318
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, May E.
Goddard, Audrey
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
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Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
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US-09-978-697-488
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APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE SPERIES SOPPICE: 2001-10-15

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR PLILING DATE: 2001-01-730

PRIOR PLILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/065311
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                                                                                                                                                                                                                                                                                                                                                                      182 QLDLEDLYRPTWQLLGKAFVPGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT
                                                                                                   KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL
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                                                    KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL
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Mismatches
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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Napier, Mary A.
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  Matches 317; Conservative
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APPLICANT: Baker Kevin P
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R FILING DATE: 1998-04-29
R FILING DATE: 1998-04-30
R APPLICATION NUMBER: 60/08436
R FILING DATE: 1998-05-05
R FILING DATE: 1998-05-05
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084414
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/08441
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/08441
R FILING DATE: 1998-05-06
R FILING DATE: 1998-05-06
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RAPLICATION NUMBER: 60/084600
RR FILING DATE: 1998-65-07
RAPLICATION NUMBER: 60/084627
RAPLICATION NUMBER: 60/084627
RAPLICATION NUMBER: 60/084633
RFILING DATE: 1998-05-07
RAPLICATION NUMBER: 60/085339
RFILING DATE: 1998-05-13
RR FILING DATE: 1998-05-15
                                                                                             R FILING DATE: 1998-04-23

R APPLICATION NUMBER: 60/08336

R APPLICATION NUMBER: 60/08332

R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-29

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083495

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083496

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083499

R APPLICATION NUMBER: 60/083499

R APPLICATION NUMBER: 60/08345

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/08345

R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/08345
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084598
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/08580
APPLICATION NUMBER: 60/085573
                      APPLICATION NUMBER: 60/082797
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
FILING DATE: 1998-04-29
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
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  DATE: 1998-04-22
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99.7%; Score 1728; DB 10; Length 345; 100.0%; Pred. No. 5.3e-166;

Query Match Best Local Similarity

PRIOR FILING DATE: 1997-11-21 PRIOR FILING DATE: 1998-03-10 PRIOR FILING DATE: 1998-03-10 PRIOR FILING DATE: 1998-03-11 PRIOR PELICATION NUMBER: 60/077649 PRIOR PELICATION NUMBER: 60/077691 PRIOR FILING DATE: 1998-03-13 PRIOR PELICATION NUMBER: 60/078016 PRIOR FILING DATE: 1998-03-23 PRIOR FILING DATE: 1998-03-23 PRIOR FILING DATE: 1998-03-20 PRIOR FILING DATE: 1998-03-27 PRIOR PELICATION NUMBER: 60/079569 PRIOR PELICATION NUMBER: 60/079669 PRIOR FILING DATE: 1998-03-27 PRIOR PELICATION NUMBER: 60/079669 PRIOR FILING DATE: 1998-03-27 PRIOR PELICATION NUMBER: 60/079020 PRIOR PELICATION NUMBER: 60/080105 PRIOR PELICATION NUMBER: 60/080105 PRIOR PELICATION NUMBER: 60/080134 PRIOR PELICATION NUMBER: 60/080																																																				
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PRIOR APPLICATION NUMBER: 60/081938
PRIOR FILING DATE: 1998-04-15
PRIOR FILING DATE: 1998-04-21
PRIOR FILING DATE: 1998-04-21
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-06
PRIOR PLING DATE: 1998-05-07
PRIOR

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TLE OF INVENTION: Acids Encoding the Same LE REFERENCE: P2630P1C63
                                                      CURRENT APPLICATION NUMBER: US/09/999,832A CURRENT FILING DATE: 2001-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR PELING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-25
PRIOR PELING DATE: 1998-03-25
PRIOR PELING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079659
PRIOR APPLICATION NUMBER: 60/079664
PRIOR APPLICATION NUMBER: 60/079669
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079669
PRIOR FILING DATE: 1998-03-27
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PRIOR APPLICATION NUMBER: 60/07969
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07969
PRIOR PILING DATE: 1998-03-37
PRIOR APPLICATION NUMBER: 60/080105
PRIOR PILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080105
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-04-01
                                                                                                 PRIOR APPLICATION NUMBER: 09/91818
PRIOR PILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-110-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-10
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R FAPLICATION NUMBER: 60/077641
R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/077649
R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/07791
R FILING DATE: 1998-03-12
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APPLICATION UNDHER: 60/078886
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081071
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100.0%; Pred. No. 5.3e-166;
iive 0; Mismatches 0;
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Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Beker Kevin P.
APPLICANT: Bettein, David
APPLICANT: Bettein, David
APPLICANT: Eaton, Dan
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR PRILICATION NUMBER: 60/08574
PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085697
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerriteen, Mary E.
Goddard, Audrey
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Williams, P. Mickey
Wood, William I.
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Kuo, Sophia S.
Napier, Mary A.
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Best Local Similarity 100.'
Matches 317; Conservative
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PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION UNDER: 60/08129
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PRIOR APPLICATION UNDER: 60/08129
PRIOR PILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-20
PRIOR PILING DATE: 1998-04-20
PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-21
PRIOR PILING DATE: 1998-04-22
PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-
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149 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERR 208
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99.7%; Score 1728; DB 10;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08539
PRIOR PILING DATE: 1998-05-13
PRIOR PLING DATE: 1998-05-13
PRIOR PLING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR APPLICATION NUMBER: 60/085323
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08569
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Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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Grimaldi, J. Christopher
Gurney, Austin L.
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Goddard, Audrey
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Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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Eaton, Dan
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US-09-978-189-488
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R FILING DATE: 1998-04-01
R APPLICATION NUMBER: 60/080328
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R APPLICATION NUMBER: 60/080333
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R APPLICATION NUMBER: 60/081070
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R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/082569
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082004
R APPLICATION NUMBER: 60/082004
R APPLICATION NUMBER: 60/082700
R APPLICATION NUMBER: 60/082797
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RR FILING DATE: 1998-04-29
RR FILING DATE: 1998-04-29
RR APPLICATION NUMBER: 60/083495
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R FILING DATE: 1998-04-08
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R FILING DATE: 1998-04-09
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R APPLICATION NUMBER: 60/081955
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FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/084441
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30
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APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/083336
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/082568
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Shelton, David L.
Stewart, Timothy A.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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                                                                          Napier, Mary A.
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89 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148
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100.0%; Pred. No. 5.3e-166;
tive 0; Mismatches 0;
                        FILE REFERENCE: (253-12.7)

(CURRENT APPLICATION NUMBER: US/99/96,753

CURRENT FILING DATE: 1998-10-30

PRIOR APPLICATION NUMBER: 09/23,094

PRIOR APPLICATION NUMBER: 09/23,094

PRIOR PILING DATE: 1998-12-30

PRIOR PLILING DATE: 1998-02-26

PRIOR PLILING DATE: 1999-03-01

PRIOR PLILING DATE: 1999-05-14

PRIOR PLILING DATE: 1999-05-10

PRIOR PLILING DATE: 1999-12-29

PRIOR PLILING DATE: 2000-05-14

PRIOR PLILING DATE: 2000-05-14

PRIOR PLILING DATE: 2000-05-16

PRIOR PLILING DATE: 2000-05-19

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Best Local Similarity 100.0
Matches 317; Conservative
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ORGANISM: Homo sapiens
US-09-796-753-6
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Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: ACCATEN, Sean A.
IITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR APPLICATION NUMBER: 60/084640
PRIOR APPLICATION NUMBER: 60/084590
PRIOR FILING DATE: 1998-05-07
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR PELING DATE: 1998-5-07
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PRIOR PILING DATE: 1998-05-07
PRIOR PILING DATE: 1998-05-13
PRIOR PILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08558
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
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                 149 YFPSERGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 208
                                                                               242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
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122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181
                                                            182 QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT 241
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99.7%; Score 1728; DB 11; Length 345;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 317; Conservative 0; Mismatches 0; Indels 0;
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CURRENT PPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
                                                                                                                                                                                                                                                                                                     Sequence 488, Application US/09978608A Publication No. US20030045462A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Stewart, Timothy A.
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Kljavin, Ivar J.
Kuo, Sophia S.
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Filvaroff, Ellen
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Eaton, Dan
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LENGTH: 345
TYPE: PRT
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89 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 148
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P263.0PLC15
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
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Grimaldi, J. Christopher
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Shelton, David L.
Stewart, Timothy A.
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gerber, Hanspeter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baker Kevin P.
Botstein, David
Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ashkenazi, Avi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eaton, Dan
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Db 89 TFDERFGLEDPEDDICKYDFVEVEFSALPLDLIANAITAFSTLEDLIRYLEPERM 181

Db 122 YFPSEPGFCHTYNIVMPQFTEAVSPSVLPPSALPLDLIANAITAFSTLEDLIRYLEPERM 181

149 YFPSEPGFCHTYNIVMPQFTEAVSPSVLPPSALPLDLIANAITAFSTLEDLIRYLEPERM 208

Qy 182 QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLTTEEVRLYSCTPRNFSVSIRBELKRTDT 241

Db 209 QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLTTEEVRLYSCTPRNFSVSIRBELKRTDT 268

Qy 242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHBVLQLRFYRGTRGLKRSLTDVA 301

Db 269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHBVLQLRFYTGVRGLHKSLTDVA 328

Qy 302 LEHHEECDCVCRGSTGG 318

Db 329 LEHHEECDCVCRGSTGG 345
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Search completed: November 25, 2003, 21:17:05 Job time : 23.3988 secs

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Sequence 4, P Sequence 3, P Sequence 2, P Sequence 2, Sequence 2, Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli

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32, Appl 2, Appli 2, Appli 2, Appli 149, App

Sequence

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Sequence 51, Sequence 32,

Sequence 2

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Perfect score:

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GENERAL INFORMATION:

GENERAL INFORMATION:

JEQUACCE 5, ADDICATION OF CANCER RESEARCH
APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH
APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER
CURRENT APPLICATION THEREFOR, AND USES THEREOF
FILE REFERENCE: PCT/US99/22669-LUDWIG INST FOR CANCER
CURRENT FILING DATE: 1999-09-30
EARLIER FILING DATE: 1998-09-30
EARLIER FILING DATE: 1998-11-2
EARLIER FILING DATE: 1998-11-2
EARLIER FILING DATE: 1998-11-03
EARLIER FILING DATE: 1998-12-03
EARLIER FILING DATE: 1998-12-03
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
1 US-09-410-349A-5

1 US-09-852-209-5

1 US-09-852-209-5

1 US-10-131-600-5

1 US-10-131-600-5

1 US-10-131-97B-5

1 US-10-131-97B-5

1 US-09-31025-29

1 US-09-31025-29

1 US-09-2456-3-4

1 US-09-2456-3-4

1 US-09-1574-2

1 US-09-1574-3

1 US-09-157-105-2

1 US-09-157-105-2

1 US-09-107-105-2

1 US-09-107-105-2

1 US-09-107-105-2

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         Sequence 5, Appli
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                          1 GKFQFSSNKEQNGVQDPQHE.....DVALEHHEECDCVCRGSTGG 318
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1: /cgn2_6/ptodata/1/paa/BCTUS COMB.pep:*
2: /cgn2_6/ptodata/1/paa/USO6_COMB.pep:*
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18: /cgn2_6/ptodata/1/paa/USO99_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/USO99_COMB.pep:*
10: /cgn2
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Compugen Ltd.
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                          version :
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                          GenCore (c) 1993
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                                                                                                                                                            November 25,
                                               Copyright
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 WQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEBVRLYSCTPRNFSVSIREELKRTD
                                                                                                                 1 GKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQ
                                                                                                                                                                                                                                                                                                                 EYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPER
                                                                                1 GKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQ
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                          Gaps
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                          Indels
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PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-09-16
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1990-07-15
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; Pred. No. 1.9e-165;
0; Mismatches 0;
  Pred. No. 1.9e-165;
                       0; Mismatches
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Sequence 5, Application US/09852209; GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: AASE, Karin
APPLICANT: LEB. Xuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ALEHHEECDCVCRGSTGG 318
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Best Local Similarity 100.0%;
Matches 318; Conservative 0
100.08;
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UUTELA, Marko
ALITALO, Kari
Best Local Similarity 100.
Matches 318; Conservative
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APPLICANT:
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APPLICANT: AASE, KARIN
APPLICANT: PONTEN, Annica
APPLICANT: PONTEN, Annica
APPLICANT: PONTEN, Annica
APPLICANT: PONTEN, Annica
APPLICANT: PIELDIN, Kari
APPLICANT: MITALO, Kari
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: HERENOT, Christer
TILLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, D
TITLE OF INVENTION: PLATERER 1990-09-30
FRIOR FILING DATE: 1999-09-30
FRIOR APPLICATION NUMBER: 60/108,109
FRIOR FILING DATE: 1998-12-03
FRIOR FILING DATE: 1998-12-18
FRIOR FILING DATE: 1998-12-18
FRIOR FILING DATE: 1999-07-15
                                                                                                                                                                                               Query Match 100.0%; Score 1734; DB 1; Best Local Similarity 100.0%; Pred. No. 1.9e-165; Matches 318; Conservative 0; Mismatches 0;
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SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 5
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                          PCT-US99-22668-5
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US-09-410-349A-5
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241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDV 300
                                                                                                        241 TIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDV 300
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Best Local Similarity 100.0%; Score 1734; DB 27; Length 318;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0; Indels 0;
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APPLICANT: OLITALO, KAZIA
APPLICANT: OESTMAN, Arne
APPLICANT: OESTMAN, Arne
APPLICANT: HELDIN, CAT'I therrik
APPLICANT: HELDIN, CAT'I-therrik
APPLICANT: BELSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREPOX, AND USES THERROP
TITLE OF INVENTION: THEREPOX, AND USES THERROP
TITLE OF INVENTION: 074-25
FILE REFERENCE: 09-410349-Exikason et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/410,349
FRIOR APPLICATION NUMBER: 60/110,749
FRIOR FILING DATE: 1998-12-03
FRIOR APPLICATION NUMBER: 60/113,002
FRIOR APPLICATION NUMBER: 60/113,002
FRIOR PRILING DATE: 1998-12-18
FRIOR APPLICATION NUMBER: 60/113,002
FRIOR FILING DATE: 1999-05-21
FRIOR PRILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-07-15
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GENERAL INFORMATION:
APPLICANT: BRIKSSON, Ulf
                                                                                                                                                                        301 ALEHHEECDCVCRGSTGG 318
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UUTELA, Marko
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LEE, Xuri
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US-10-131-600-5
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LIFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD
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APPLICANT: HELDIN, CAI-Henrik
APPLICANT: HERDIN, CAI-Henrik
APPLICANT: HERDIN, CAI-Henrik
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TORRENT APPLICATION NUMBER: US/09/852,209A
CURRENT APPLICATION NUMBER: 09/410,349
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1999-10-03
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOSTWARRE: PATCHTIN VOY: 2.0
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100.0%; Score 1734; DB 23;
Best Local Similarity 100.0%; Pred. No. 1.9e-165;
Matches 318; Conservative 0; Mismatches 0;
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ALITALO, Kari
OESTMAN, Arne
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ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-852-209A-5
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TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS ENCODING THEM
FILE REPERENCE: 7853-173
CURRENT APPLICATION NUMBER: US/09/471,179
CURRENT FILING DATE: 1999-12-23
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
ENGTH: 323
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 323;
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILE REFERENCE: 7853-13-228
CURRENT APPLICATION NUMBER: PCT/US99/31025
CURRENT PILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: 99/23, 546
SEALLIER PILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.7%; Score 1728; DB 1;
Best Local Similarity 100.0%; Pred. No. 8e-165;
Matches 317; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 8e-165;
Matches 317; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
PCT-US99-31025-29
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US-09-471-179-29
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### GENERAL INFORMATION:

### APPLICANT: L1, Xuri

### APPLICANT: CARMELIET, Peter

### APPLICANT: COLONDOR: COMPOSITION NUMBER: US/10/303,997B

### APPLICANT: US/10/303,997B

#### APPLICANT: US/10/3
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PCT-US99-31025-29
F. Sequence 29, Application PC/TUS9931025
; GENERAL INFORMATION:
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                                                           301 ALEHHEECDCVCRGSTGG 318
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Best Local Similarity 100.
Matches 318; Conservative
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                                                                                                                                                                                                                   RESULT 6
US-10-303-997B-5
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT FILING DATE: 203-10-20
PRIOR PELICATION NUMBER: 60/049911
PRIOR PLING DATE: 1997-06-18
PRIOR PLING DATE: 1997-06-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-19
PRIOR PLING P
                                                                                                                                                                                                                          187 QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT 246
                                                                                                                                                                                                                                                                                                                                                247 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 306
                                                                                                                     127 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLBPERW 186
                                                                                                                                                                                   OLDLEDLYRPIWOLLGKAFVFGRKSRVVDLNLLTBEVRLYSCTPRNFSVSIREELKRTDT 241
                                                          YPPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181
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PET-USO1-43523-286

Sequence 286, Application PC/TUS0143523

GENERAL INFORMATION:
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Smith, Victoria
Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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; ORGANISM: Homo Sapien
PCT-US01-43523-286
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APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330R.10331
CURRENT APPLICATION NUMBER: PCT/USO2/24563
CURRENT FILING DATE: 2002-08-02
PRIOR PLING DATE: 1997-06-18
PRIOR FILING DATE: 1997-06-18
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-18
PRIOR PLING DATE: 1997-09-18
PRIOR PLING DATE: 1997-09-18
PRIOR PLING DATE: 1997-09-18
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                                                                                                                                                                                                                                                                                                                                                                    208
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                                                                                                                                                                                                         62 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
                                                                                                                                                                                                                                                                                                                122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181
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                                                                                                       61
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                                                                                                    2 KPQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTXPRNTVLVWRLVAVEENVWIQL
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  Length 345;
                                                Indels
99.7%; Score 1728; DB 1; Lilarity 100.0%; Pred. No. 8.8e-165; Conservative 0; Mismatches 0;
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Stewart, Timothy A.
Tumas, Daniel
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Gurney, Austin L.
Sherwood, Steven
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Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Filvaroff, Ellen
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  Query Match
Best Local Similarity
Matches 317; Conserv
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PCT-US99-01574-2
Sequence 2, Application PC/TUS9901574A
Sequence 2, Application PC/TUS9901574A
GENERAL INFORMATION:
APPLICANT: Song, Ho Yeong
APPLICANT: Dou, Shenshen
TITLE OF INVENTION: VEGF Related Gene and Protein
FILE REPERENCE: X-11851
CURRENT APPLICATION NUMBER: PCT/US99/01574A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver: 2.0
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TILLE OF INVENTION: Bone Morphogenic Protein
FILE REFERENCE: PT012.PCT
CURRENT APPLICATION NUMBER: PCT/US99/15783
CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,922
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Matches 317; Conservative
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PCT-US99-15783-4
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TYPE: PRT
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; Sequence 344, Application PC/TUS0304213
; GENERAL INFORMATION:
    APPLICANT: ZymoGenetics, Inc.
    TITLE OF INVENTION: MATERIALS AND METHODS FOR PREPARING DIMERIC GROWTH FACTORS
    FILE REPERENCE: 01-33PC
    CURRENT APPLICATION NUMBER: PCT/US03/04213
    CURRENT PILING DATE: 2003-02-11
    PRIOR PILING DATE: 2003-02-11
    NUMBER OF SEQ ID NOS: 34
    SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 34
    LENGTH: 345
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PRIOR FILING DATE: 1997-05-15
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 297-09-19
PRIOR APPLICATION NUMBER OF SEQ ID NOS: 550
SEQ ID NO 286
LENGTH: 345
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100.0%; Pred. No. 8.8e-165;
iive 0; Mismatches 0;
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100.0%; Pred. No. 8.8e-165;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 317; Conservative
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Best Local Similarity 100.
Matches 317; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo Sapien
PCT-US02-24563-286
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PCT-USS9-31025-2
FGQUENCE 2, Application PC/TUS9931025
GGNERAL INFORMATION:
APPLICANT: Millennium Pharmaceticals, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND NUCLEIC ACIDS
TITLE OF INVENTION: ENCODING THEM
FILLE REPERBREE: 7853-173-228
GURRENT APPLICATION NUMBER: PCT/US99/31025
GURRENT FILING DATE: 1999-12-238
FARLIER PPLICATION NUMBER: 09/223,546
FARLIER FILING DATE: 1999-12-33
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO: 345
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APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.
ITILE OF INVENTION: PLATELET DERIVED GROWTH FACTOR C,
ITILE OF INVENTION: PLATELET THEREOF
ITILE REPERBENCE: PCT/US99/22669-LUDWIG INST FOR CANCER
CURRENT APPLICATION NUMBER: PCT/US99/22668B
CURRENT APPLICATION NUMBER: 60/102,461
EARLIER APPLICATION NUMBER: 60/102,461
EARLIER APPLICATION NUMBER: 60/109,109
EARLIER PILING DATE: 1998-09-30
EARLIER PILING DATE: 1998-11-12
EARLIER PILING DATE: 1998-11-3
EARLIER FILING DATE: 1998-12-3
EARLIER FILING DATE: 1999-12-18
EARLIER FILING DATE: 1999-12-18
EARLIER FILING DATE: 1999-12-18
EARLIER APPLICATION NUMBER: 60/113,002
EARLIER PILING DATE: 1999-0-12
EARLIER APPLICATION NUMBER: 60/114,022
EARLIER APPLICATION NUMBER: 60/144,022
EARLIER PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SEQ ID NO 3
IEBNGTH: 345
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Best Local Similarity 100.0%; Pred. No. 8.8e-165;
Matches 317; Conservative 0; Mismatches 0;
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  EARLIER FILING DATE: 1998-07-15
                        NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 317; Conservative
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ORGANISM: Homo sapiens
                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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PCT-US99-22668-3
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; Search time 12.619 Seconds (without alignments) 1293.384 Million cell updates/sec November 25, 2003, 21:02:59 using sw model OM protein - protein search, Run on:

US-09-852-209A-5 1734 1 GKPQFSSNKEQNGVQDPQHE......DVALEHHEECDCVCRGSTGG 318 score: Sequence: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

271250 segs, 51324744 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 sed 88 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending_Patents_AA_New:*

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7: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMERTES	
Result No.	Score	% Query Match	Length	DB	ID	Description
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7	1728	99.7	345	ß	US-09-457-066-2	7
e	1728	99.7	345	ß	US-09-876-813-33	
4	1728	7.66	345	9	US-10-648-593-191	191
Ŋ	1728	99.7	345	9	US-10-471-221-1	1, A
9	1728	7.66	345	7	US-60-487-610-1644	164
7	1728	7.66	345	7	US-60-485-450-1042	
80	1720	99.2	345	'n	US-09-830-320A-4	4. App
σ	1559	89.9	345	'n	US-09-457-066-43	Sequence 43, Appl
10	1559	89.9	345	ß	US-09-876-813-35	35
11	1325	76.4	302	5	US-09-876-813-54	54
12	1320.5	76.2	282	9	US-10-471-221-5	Ŋ,
13	1266.5	73.0	303	ß	US-09-876-813-57	Sequence 57, Appl
14	1107	63.8	305	٦	PCT-US00-28803-7	7
15	1098	63.3	316	Ŋ	US-09-876-813-55	55
16	1051.5	9.09	317	'n	5	26
17	741	42.7	370	ß	US-09-457-066-37	37
	741	42.7	370	ß	-03-876-	7
	741	42.7	370	9	-10-	4
	741	42.7	370	9	US-10-606-055-2	7
	736	42.4	370	ഹ	US-09-876-813-53	Sequence 53, Appl
22	736	42.4	370	9	US-10-321-962-8	8
23	736	42.4	370	9	US-10-606-055-4	4
	684	39.4	167	9	US-10-471-221-6	9
25	604	34.8	111	ø	-10-471-	7
26	431	24.9	261	9	US-10-321-962-10	Sequence 10, Appl

Appli	, Appl	2251, Ap	12, Appl	2257, Ap	2260, Ap	2268, Ap	14, Appl	2259, Ap	2266, Ap	2267, Ap	1841, Ap		2252, Ap		2263, Ap	242, App	54, Ap	2264, Ap
Seguence 6,	Sequence 12	Sequence 22	Sequence 12	Seguence 22		Seguence 22	Sequence 14	Sequence 22	Sequence 22	Sequence 22		Sequence 22	Sequence 22	Sequence 22	Sequence 22		Sequence 22	Seguence 22
US-10-321-962-6	US-10-321-962-12	US-60-495-114-2251	US-09-830-320A-12	US-60-495-114-2257	US-60-495-114-2260	US-60-495-114-2268	US-10-321-962-14	US-60-495-114-2259	US-60-495-114-2266	US-60-495-114-2267	US-60-495-114-1841	US-60-495-114-2262	US-60-495-114-2252	US-60-495-114-2253	US-60-495-114-2263	US-10-474-794-242	US-60-495-114-2254	US-60-495-114-2264
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328.5	320.5	187	181.5	181.5	181.5	181.5	174	173	173	173	171	169	169	169	169	169	169	169
27	28	59	30	33	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
FILLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILLE REFERENCE: D0273 PCT
CURRENT APPLICATION NUMBER: PCT/US03/26491
CURRENT PILLING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: Patentin version 3.2
SGOID NO 191
LENGTH: 345
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                                    Sequence 191, Application PC/TUS0326491 GENERAL INFORMATION:
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RESULT 1
PCT-US03-26491-191
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GENERAL INFORMATION:

APPLICANT: dav, Zeren

APPLICANT: Hart, Charles E.

APPLICANT: Hart, Charles E.

APPLICANT: Hack, Charles E.

APPLICANT: APPLICANT: Sheepard, Paul O.

APPLICANT: Sheemaker, Kimberly E.

APPLICANT: Glabertson, Debra G.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

TITLE OF INVENTION: 28-6

CURRENT APPLICATION NUMBER: US/09/457,066

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                  99.7%; Score 1728; DB 5; L 100.0%; Pred. No. 2.8e-139; ive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Glibert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: APPLICANT: Brepard, Paul O.
TITLE OF INNENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/876,813
CURRENT FILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
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Matches 317; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP
CURRENT PILLOGATION NUMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: Patentin version 3.2
SEQ ID NO 191
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Pred. No. 2.8e-139;
                                                                                                                                                                                                99.7%; Score 1728; D 100.0%; Pred. No. 2.8 tive 0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 33 LENGTH: 345
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Best Local Similarity 100.
Matches 317; Conservative
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; ORGANISM: Homo sapiens
US-10-648-593-191
                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 317; Conserv
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US-10-648-593-191
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US-09-876-813-33
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100.0%; Pred. No. a...
... 0; Mismatches
 NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 317; Conservative
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US-60-485-450-1042
                                                                TYPE: PRT
ORGANISM: Homo
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                                SEQ ID NO 1644
LENGTH: 345
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GREEAL INFORMATION:
APPLICANT: CREGILL, Michele
APPLICANT: HUANG, Horajin
TITLE OF INVENTION: GREETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: C1001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
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GENERAL INFORMATION:
APPLICANT: Jansenn Pharmaceutica N.V.
TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
FILE REFERENCE: JAB 1687
CURRENT APPLICATION NUMBER: US 10/471,221
CURRENT FILING DATE: 2003-09-05
FRIOR APPLICATION NUMBER: US 60/274901
FRIOR APPLICATION TOMBER: US 60/274901
FRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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100.0%; Pred. No. 2.8e-139;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 317; Conservative
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US-60~487-610-1644
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US-10-471-221-1
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APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: THEROF
TITLE OF INVENTION: THEROF
FILE REFERENCE: CLOO1470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 345
TTPE: PRT
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                                                   Indels
Score 1728; DB 7; L
Pred. No. 2.8e-139;
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89 TFDERFGLEDPEDDICKYDFVEVEEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDE 148
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87.1%; Pred. No. 6.7e-125;
ive 26; Mismatches 15; Indels
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GENERAL INFORMATION:
APPLICANT: dilbert Teresa
APPLICANT: dilbert Teresa
APPLICANT: Beppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4;
FILE REPRENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/56,813
CURRENT FILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 00/164,463
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APPLICANT: Hart, Charles E.

APPLICANT: Hidington, Christopher S.

APPLICANT: Shegbard, Paul O.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Gilbertson, Debra G.

APPLICANT: West, James W.

TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVE

FILE REFERENCE: 98-60

CURRENT PEPLICATION NUMBER: US/09/457,066

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 43

LENGTH: 345
                                                                                                                                                                                 ; Sequence 43, Application US/09457066; GENERAL INFORMATION:
                           329 LEHHEBCDCVCRGSTGG 345
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Best Local Similarity 87.1;
Matches 276; Conservative
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US-09-457-066-43
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US-09-876-813-35
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                              QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT 241
                                                                                                                                  242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
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APPLICANT: HILLMAN, Jennifer L.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: GUEGLER, Karl J.
APPLICANT: GUEGLER, Karl J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUCHN, MAREN E.
TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES
FILE REFERENCE: PF.0627 USN
CURRENT APPLICATION NUMBER: DC7/US99/25458
FRIOR FILING DATE: 1999-10-28
FRIOR APPLICATION NUMBER: US 60/183,024
FRIOR FILING DATE: 1999-10-18
FRIOR APPLICATION NUMBER: US 60/155,216
FRIOR FILING DATE: 1999-121
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1larity 99.7%; Pred. No. 1.3e-138;
Conservative 0; Mismatches 1;
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; OTHER INFORMATION: Incyte ID No.: 4163378CD1
US-09-830-320A-4
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4, Application US/09830320A; GENERAL INFORMATION: APPLICANT: INCYTE GENOMICS, INC.
                                                                                                                                                                                                                                     LEHHEECDCVCRGSTGG 318
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YUE, Henry
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Best Local Similarity
Matches 316; Conserva
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APPLICANT:
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61 YDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMP 120
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                                                                                                                                                                                                                                                                     199 AFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA 258
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                                                                                                                                                                                                                                                                                                                                                                                      240 CGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERCDCIC 296
                                                                                                                                                                                                                                                                                                                                                                 259 CCLHNCNECQCVPSKVTKKYHEVLQLRP---KTGVRGLHKSLTDVALEHHEECDCVC 312
19 HERIITVSTNGSIHSPRFPHTYPRNTVLVMRLVAVEENVWIQLTFDERFGLEDPEDDICK
                         1 HERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVBENVWIQLTFDERFGLEDPEDDICK
                                                                                         79 YDFVBVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDBYFPSEPGFCIHYNIVMP
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| Sequence 5, Application US/10471221
| Sequence 5, Application US/10471221
| GENERAL INPORMATION:
| TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
| TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
| TITLE OF INVENTION: MODER: US/10/471,221
| CURRENT APPLICATION NUMBER: US/10/471,221
| CURRENT FILING DATE: 2001-03-09
| PRIOR APPLICATION NUMBER: US 60/274901
| PRIOR FILING DATE: 2001-03-09
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: Patentin Version 3.1
| SEQ ID NO 5
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ORGANISM: Homo sapiens
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US-09-876-813-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 YFPSEPGFCIHYSIIMPQVTETTSPSVLPPSSLSLDLINNAVTAFSTLEELIRYLEPDRW 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269 IFWPGCLLVKRCGGNCACCLANCNECQCVPRKVTKKYFEVLQLRPKTGVKGLHKSLTDVA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                62 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDB 121
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                                                                                                                                                                                                                                                    Length 345;
                                                                                                                                                                                                                                                Query Match 89.9%; Score 1559; DB 5; Length 3 Best Local Similarity 87.1%; Pred. No. 6.7e-125; Matches 276; Conservative 26; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANI: JAIDELL, Charles E.
APPLICANI: HART, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION GROWTH FACTOR HOMOLOG ZVEGF4
FILE REPERENCE: 99-19
CURRENT FILING DATE: 2001-66-66
PRIOR PPLICATION NUMBER: US 09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR PLING DATE: 1999-05-03
PRIOR PLING DATE: 1999-05-03
PRIOR PLING DATE: 1999-10-10
PRIOR PLING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54
LENGTH: 302
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 345
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GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
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ORGANISM: Artificial Sequence
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Matches 246; Conservative
                                                                                                                                                         TYPE: PRT
CORGANISM: Mus musculus
US-09-876-813-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 OFTEAV-----SPSVLPPSALPLDLIANAITAFSTLEDLIRYLEPERWQ 182
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                                                                                                                                                                                                                                                                                     Length 305;
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                                                                                                                                                                                                                                                                                 Ouery Match 63.8%; Score 1107; DB 1;
Best Local Similarity 100.0%; Pred. No. 1.6e-86;
Matches 206; Conservative 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OLDLEDLYRPTWOLLGKAFVFGRKSR 234
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                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-09-876-813-55
                                                                                                                                                                                                               PCT-US00-28803-7
                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 LIGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWFGCLLVKRCG 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 DFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCHYNIVM 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 DETIQUKGNGYVQSPRFPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDICRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 ERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKY
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GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Donoho, Gregory
APPLICANT: Nehls, Michael
APPLICANT: Mehls, Michael
APPLICANT: Mehls, Michael
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
ITLE OF INVENTION: Novel Human Proteins and Polynucleotides
ITLE OF INVENTION: Brooding the Same
ITLE OF INVENTION: NOWBER: PCT/US00/28803
CURRENT FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.0%; Score 1266.5; DB 5; Length 303; 78.9%; Pred. No. 4.3e-100; ive 24; Mismatches 33; Indels 7;
                         APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF4
FILE REPERENCE: 99-19
CURRENT PILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US/09/564,595
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR PLICATION NUMBER: US 09/304,216
PRIOR PLILNG DATE: 1999-05-03
PRIOR PLILNG DATE: 1999-05-03
PRIOR PLILNG DATE: 1999-05-04
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE FASELSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 78.9%
Matches 240; Conservative
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November 25, 2003, 20:59:34; Search time 13.5655 Seconds (without alignments) 2254.373 Million cell updates/sec Run on:

US-09-852-209A-5

1734 1 GKFQFSSNKEQNGVQDPQHE.....DVALEHHEECDCVCRGSTGG 318 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

metalloproteinase complement subcomp Ra-reactive factor polyprotein - Afri henain - rabbit vascular endotheli hypothetical prote platelet-derived g hyaluronate-bindin platelet-derived g tumor necrosis fac TSG-6 homolog PS4 intrinsic factor-B procollagen C-endo procollagen C-endo procollagen C-endo intrinsic factor-B procollagen I C-pr dorsal-ventral pat spinal cord-derive spinal cord-derive procollagen C-endo A5 antigen precurs procollagen C-endo development protei procollagen I C-pr hypothetical prote Ra-reactive factor tolloid-BMP-1 like Description SUMMARIES JC7591 JC7592 JC7592 JC90948 JC2218 J S58984 JH0403 T30018 T22812 JS0735 A41735 Query Match Length DB 742 181.36 179.5 179.5 173.5 173.5 169 169 169 1139.5 139.5 139.5 131.5 Result No.

membrane-type friz	16K vascular endot	platelet-derived g	platelet-derived g	platelet-derived g	platelet-derived g	UVS.2 protein - Af	sanko - human	platelet-derived g	platelet-derived g	PDGF-related trans	platelet-derived g	vascular endotheli	platelet-derived g	platelet-derived g	protein F57C12.1 [
JC7629	D49530	PFHUG2	151551	S08220	151550	151569	A59386	JN0248	\$25096	TVMVSS	A37359	A41551	B28964	PFHUG1	D89447
N	N	H	C)	N	7	7	~	N	7	н	0	0	N	7	N
579	148	241	200	215	226	319	2403	166	197	226	196	232	196	211	770
6.7	9.9	9.9	6.5	6.5	6.5	6.4	6.4	6.3	6.3	6.3	6.2	6.0	6.0	6.0	6.5
16.5	114.5	114.5	112.5	112.5	112.5	111.5	110.5	110	109	108.5	108	104.5	104	104	103
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ALIGNMENTS

RESULT

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Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
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31.6%; Pred. No. 2.7e-07;
ive 29; Mismatches 73
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Best Local Similarity 31.6<sup>5</sup>
Matches 55, Conservative
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Best Local Similarity
Matches 50; Conserv
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C;Species: Homo sapiens (man)
C;Accession: A37278; ES8788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew Science 242, 1288-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730; PMID:3201241
A;Residues: 1-730 *WOZ
A;Residues: 1-730 *WOZ
A;Cross-references: GB:M22488; NID:g179499; PIDN:AA51833.1; PID:g179500
C;Genetics:
A;Gene: GDB:BMP1
A;Cross-references: GDB:125203; OMIM:112264
A;Map position: Sp21-8p21
C;Function:
A;Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen type C;Superfamily: procollagen C-endopeptidase; astacin homology; CIr/CIs repeat homology; E
spinal cord-derived growth factor-B precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001 C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001 C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001 S;Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y. Biochem. Biophys. Res. Commun. 280, 733-737, 2001 A;Title: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C/A;Reference number: JOT991; MUID:21092670; PMID:11162582
                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA
A,Residues: 1-370 cHAM>
A,Cross=references: DDBJ:AB052170
C,Genetics: codf-B
A,Gene: scdgf-B
F;1-17/Domain: secretory signal sequence #status predicted <SIG>F;1-17/Domain: secretory signal cord-derived growth factor-B #status predicted <WAT>F;2-1-70/Region: CUB domain #status predicted F;2-2-70/Region: homologous to platelet-derived growth factor/vascular endothelial grow F;294-3308/Region: conserved motif #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECOCVPSKVTKKYHEVLQLRP-- 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | | : | : | || || || ESNHLTDLYRRDENIRVTGTGHVQSPRFPNSYPRNLLLTWRLHS-QEKTRIQLAFDHQFG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEDPEDDICKYDFVEVEREPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGECIHYNIV---MPQFTEAV------SPSVLPPSALPLDLINNAITAFST 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNF 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
42.4%; Score 736; DB 2; Length 37
Best Local Similarity 45.6%; Pred. No. 3.9e-56;
Matches 149; Conservative 57; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KTGVRGLHKSLTDVALEHHEECDCVC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Contents: Fetal brain A; Accession: JC7592
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A, Moclecule type: mRNA
A, Residues: 1-927 < TAKA.
A, Cross-references: GB:D10467; GB:D01077; NID:g222962; PIDN:BAA01260.1; PID:g222963
A, Residues: 1-927 < TAKA.
A, Note: this protein has morifs homologus to complement components C1r and C1s and to C, Comment: This protein is a neuronal cell surface molecule involved in the neuronal r. C; Superfamily: Xenopus As antigen; C1r/C1s repeat homology; discoidin I amino-terminal C; Reywords: duplication; glycoprotein; transmembrane protein
C; Reywords: duplication; glycoprotein; transmembrane protein
F; 22-927/Product: As antigen #status predicted < ASGA
F; 22-138/Domain: C1r/C1s repeat homology < C1R2.>
F; 24-424/Domain: discoidin I amino-terminal homology < DN1.>
F; 340-584/Domain: discoidin I amino-terminal homology < DN2.>
F; 366-812/Domain: transmembrane #status predicted < TWM.>
F; 861-883/Domain: transmembrane #status predicted < TWM.>
F; 861-8 A5 antigen precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JH0466; JQ0948
C;Accession: JH0466; JQ0948
R;Takaqi, S.; Hixata, T.; Agata, K.; Mochii, M.; Equchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
Neuron 7, 295-307, 1991
A;Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologate ference number: JH0466; MUID:91337458; PMID:1908252 Fig. 22/Domain: signal sequence #status predicted <SIG>
Fig. 22/Domain: signal sequence #status predicted <SIG>
Fig. 3-730/Product: procollagen C-endopeptidase splice form BMPI #status predicted <MAT>
Fig. 3-731/Domain: astacin homology <AST>
Fig. 3-731/Domain: cir/Cis repeat homology <CIRI>
Fig. 554-547/Domain: Cir/Cis repeat homology <CIRI>
Fig. 551-587/Domain: EGF homology <EGR>
Fig. 1.42, 332, 363, 599/Binding site: carbohydrate (Asn) (covalent) #status predicted Fig. 3-19, 185-205, 322-348, 375-397, 435-461, 488-510, 551-563, 559-572, 574-587, 591-617, 644-17, 232, 272/Binding site: carbohydrate (Asn) #status predicted Fig. 3-19, 186-205, 322-348, 375-397, 435-461, 488-510, 551-563, 559-572, 574-587, 591-617, 644-17, 232, 272/Binding site: zinc (His, His, His, Tyr) #status predicted Fig. 4-10, 400-400 site: Glu #status predicted Fig. 4-10, 400-400 site: 7; EV -- EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMP-- 138 EVIDGDNANGQLLGKYCGK-IAPSPLVSTGPSIFIRFVSDYETPG-AGFSIRYEVFKTGP 145 87 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV 144 82 87 98 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 28 NGSIHSPREPHTYPRNIVLVWRLVA-VEENVWIQLIFDERFGLEDPEDDICKYDFVEVEE 17; 17; Length 927; ch 10.5%; Score 181.5; DB 1; Length 730; Similarity 37.3%; Pred. No. 1.3e-07; 50; Conservative 20; Mismatches 47; Indels 17 Indels

1067

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A,Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen tyl C,Superfamily: procollagen C-endopeptidase; astacin homology; CIr/CIs repeat homology; C,Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; f;1-22/Domain: signal sequence #status predicted <SIG>
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-823/Froduct: procollagen C-endopeptidase splice form HIS #status predicted <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted F;163-319,185-205,322-348,375-397,435-461,488-510,551-563,559-572,574-587,591-617,644-(F;18,319,7122,3272/Binding site: zinc (His, His, His, Tyr) #status predicted F;214/Active site: Glu #status predicted F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ), Molecule type: mRNA

1, Molecule type: mRNA

1, Teaddues: 1-702, FRRPALQPPRGRPHQLKPRVQKRNRTPQ' < WOZ>

1, Cross-references: GB:M22488; NID:g179499; PIDN:AA51833.1; PID:g179500

1, Takadara, K.; Lyons, G.E.; Greenspan, D.S.

1, Biol. Chem. 269, 32572-32578, 1994

1, Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are enconstruction number: A59788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      procollagen C-endopeptidase (BC 3.4.24.19) precursor, splice form HIS - human NyAlternate names: bone morphogenic protein splice form BMP-1/His Cispecies: Homo sapiens (man) Cispecies: Homo sapiens (man) Cipate: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999 CiAccession: A37278, A58788 K:Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, Science 242, 1528-1534, 1988 A;Title: Novel regulators of bone formation: molecular clones and activities. A;Reference number: A37278; MUD: 89072730; PMID: 3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           968 HLIHLMF-ETFHLEFHYN--CTNDYLEVYDTDSETSLGRYCGK-SIPPSLTSSGNSLMLV 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220 -----LY--SCIPRNFSVSIREELK-RIDTI------FWPGCLLVKRCGGNCACCLH 262
                                                                                                                                                                                 57 VWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 FVSDRYFPSEPGFCIHYNIV------MPOFTEAVSPSVLPPSALPLDLLNNAITAFSTLE 170
                                                                                                                         3 PQFSSNKEQNG-----VQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Molecule type: mRNA
A,Residues: 703-823 «TAK»
A,Cross-references: GB:L35278; NID:g619423; PIDN:AAC41703.1; PID:g619424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 DLIRYLBPERWQLDLEDLYR---PTWQLLGKAFVFGRKSRVVDLNLLTE--EVR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1171 TSSGTFISPNYPMPYYHSSECYWWLKSSHG-SAFELEFKDFHLEHHPNC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 NCNECOCVPSKVTKKYHE---VLQLRPKTGVRGLHKSLTDVALEHHEEC 308
Similarity 26.4%; Pred. No. 4.8e-06; 92; Conservative 39; Mismatches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;130-321/Domain: astacin homology <AST>
F;322-431/Domain: Clr/Cls repeat homology <CIR1>
F;435-544/Domain: Clr/Cls repeat homology <CIR2>
F;555-587/Domain: RGF homology <RGF>
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         Best Local Similarity
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A; Residues: 1-707 < MAB>
A; Cross-references: GB:L12249; NID:g406540; PIDN:AAA16313.1; PID:g406541
C; Comment: This protein induces ectopic cattilage formation in vivo.
C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cis repeat homology; C; Superfamily: beta-hydroxyasparagine; glycoprotein; hydrolase; metalloproteinase; zinc F; 93-284/Domain: clr/Cis repeat homology < AST>
F; 285-394/Domain: clr/Cis repeat homology < Clr:
F; 396-510/Region: complement lr/1s-like repeat
F; 396-510/Domain: Clr/Cis repeat homology < Clr:
F; 554-66/Region: complement lr/1s-like repeat
F; 554-66/Region: complement lr/1s-lik
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
C;Accession: T09456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
                                                                                                                                                                                                                                                        procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN)
NyAlternate names: bone morphogenic protein 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
C;Accession: JC2218
R;Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A;Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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A;Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      562 NGSINSPGWPKEYPPNKNCIWQLVAPIQ-YRISLKFDQ---FETEGNDVCKYDFVEVRSG 617
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C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F;1-24/Domain: Bignal sequence #status predicted <SIG>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
F;35-3623/Product: EGF homology <EGF>
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10.1%; Score 176; DB 2; Length 707;
Best Local Similarity 43.3%; Pred. No. 3.8e-07;
Matches 45; Conservative 15; Mismatches 36; Indels
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A;Accession: T09456
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-3623 <K
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DB 2; Length 3623;

10.0%; Score 173.5;

Query Match

C; Genetics:

R.W.; H.

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C; Accession: 149540

R; Piktagawa, M; Noboru, S.; Hogan, B.L.M.; Jones, C.M.

R; Piktagawa, M; Noboru, S.; Hogan, B.L.M.; Jones, C.M.

R; Piktagawa, M; Noboru, S.; Hogan, B.L.M.; Jones, C.M.

A; Attiel: Embryonic expression of mouse bone morphogenetic protein-1 (EMP-1) which is re
A; Reference number: 149540; MUID:94229342; PMID:8174772

A; Recession: 149540

A; Recession: 149540

A; Recession: 149540

A; Residues: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRWA

A; Residues: 1-991 <RES

A; Molecule type: mRWA

A; Residues: 1-991 <RES

A; Cross-references: GB:L24755; NID:9439606; PIDN:AAA37306.1; PID:9439607

C; Genetics:
A; Gene: Emp-1

C; Superfamily: procollagen C-endopeptidase; astacin homology; CIr/CIs repeat homology; CS Keywords: hydrolase; metalloproteinase; zinc

F; SSG-705, Domain: EGF homology <AST>
F; SSG-705, Domain: EGF homology <AST>
F; SSG-705, Domain: EGF homology <BG2>
F; SSG-705, Domain: EGF homology <BG2>
F; SSG-705, Active site: Glu #status predicted
F; 218, 222, 228, 277, Bainding site: zinc
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C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-30/3/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F;133-164/Domain: BGF homology <BGF>
F;436-467/Domain: BGF homology <BGF>
                                                                                                                                                                                                                                 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5,
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A;Rolecule type: mRNA
A;Residues: 1-3623 <MOE>
A;Residues: 1-3623 <MOE>
A;Coss-references: EMBL:AF0222247; NID:g3834379; PIDN:AAC71661.1; PID:g3834380
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 OFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 133
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654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700
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ilarity 39.4%; Pred. No. 2.4e-06;
Conservative 17; Mismatches 39;
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les 43; Conserv
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Cippecies: Homo sapien
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                                                                                                                                                                                                                                 87 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV 144
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                                                                                                                                                                              28 NGSIHSPRFPHTYPRNTVLVMRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 86
                                                                                                     Gaps
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                     ; DB 1; Length 823;
8.4e-07;
thes 49; Indels
                         Query Match
10.0%; Score 173; DB
Best Local Similarity 35.6%; Pred. No. 8.4e-
Matches 52; Conservative 19; Mismatches
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R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, P. Astures 386, 506-510, 1997
A;Title: A second scrine protesse associated with mannan-binding lectin that activates A;Reference number: A59271; MUID:97242412; PMID:9087411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;72-90,142-156,152-165,167-180,184-211,241-259,300-348,328-361,366-412,396-430,434-55<sup>2</sup>
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C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement factor

C; Superfamily: complement subcomponent pathway; duplication; hydrolase; serine

C; Keywords: beta-hydroxyasparagine; complement pathway; duplication; hydrolase; serine

F; 1-15/Domain: signal sequence #status predicted <2GS-

F; 16-444,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>

F; 19-134/Domain: Clr/Cls repeat homology <CIRI>

F; 184-293/Domain: Clr/Cls repeat homology <CIRI>

F; 306-31/Domain: complement factor H repeat homology <FHI>

F; 366-430/Domain: complement factor H repeat homology <FHI>
                      R;Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B. Cell 67, 469-481, 1991
A;Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone A;Reference number: A39288; MUID:92034970; PMID:1840509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: A59271; Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ra-reactive factor (EC 3.4.21.-) 2 precursor - human NiAlternate names mannose binding protein-associated serine proteinase 2 (MASP-2) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      472 LKLTKDQSIDSPNYPMDYMPDKECVWRITA-PDNHQVALKF-QSFELE--KHDGCAYDFV 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Note: parts of this sequence, including the amino end of the mature protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;900-1013/Domain: CIr/CIs repeat homology <CIR5>
F;221,225,231,280/Binding site: zinc (His, His, His, Tyr) #status predicted
F;222/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVBENVWIQLTFDERFGLEDPEDDICKYDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-686 <JEN>
A;Cross-references: GB:V09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 EVEE -- PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:: || :: || || EIRDGNHSDSRLIGRFCGDKLPPNIK-TRSNQMYIRFVSD 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.6%; Score 148.5; DB 1;
Best Local Similarity 38.0%; Pred. No. 0.00015;
Matches 38; Conservative 20; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        787-896/Domain: Clr/Cls repeat homology <ClR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :445-679/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: GDB:6071500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecule type: mRNA
Accession: A39288
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C;Superfamily: Clr/Cls repeat homology
C;Superfamily: Clr/Cls repeat homology
C;Superfamily: Clr/Cls repeat homology
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-449/Product: #status predicted <MAT>
F;26-449/Product: #status predicted <MAT>
F;27-146/Domain: Clr/Cls repeat homology <CIRI>
F;159-270/Domain: Clr/Cls repeat homology acid (Gln) (in mature form) #status predicted
F;26/Modified site: pyrrolidone carboxylic acid (Gln) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A39288
dorsal-ventral patterning protein tolloid (BC 3.4.24.-) - fruit fly (Drosophila melanoga
C,Species: Drosophila melanogaster
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       procollagen I C-proteinase enhancer protein precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 06-reb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C;Accession: A55362
R;Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show J. Biol. Chem. 269, 26280-26285, 1994
J;Biol. Chem. 269, 26280-26285, 1994
J;Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, FA;Reference number: A55362; MUID:9501462; PMID:7523404
                                                                                                                                             975 SS-FYLEFHYN--CTNDYLEIYDTAAQTFLGRYCGR-SIPPSLTSNSNSIKLIFVSDSAL 1030
                                                                                                                                                                                                                                                                                                                     1090 FTDF-TLEDYFGSQCVDFVE-----IRDGGYETSPLVG---IY--CGSVLPPTIISHS 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----YWDGS--STGCGGN----LITPIGVLTS 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFT--- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 AVSDDSRRIGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAKE 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 VRLY-----SCTPRNFSVSIRBELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 GTLTTPNWPESDYPPGISCSWHIIAPPDQV-IALTF-EKFDLE--PDTYCRYDSVSVFNG 223
    324 KFSSDKLECG-----EVLTAST-GIIESPGHPNVYPRGVNCTWHVV-VQRGQLIRLEF 974
                                                                                           DERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNOIRIRFVSDEYF 123
                                                                                                                                                                                                                                                                   124 PSEPGFCIHY------LINMPOPTEAVSPSVLP--PSALPLDL------LINMAI--- 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 GSIHSPRFPHT-YPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEV---
                                                                                                                                                                                                                                                                                                                                                                                                                                            164 -TAFSTLED-----LIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNLTEB
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1179 PNYPMPYYHSSECYWRLEASHG-SPFELEFQDFHLEHHPSC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSKVTKKYHE---VLQLRPKTGVRGLHKSLTDVALEHHEEC 308
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A;Cross-references: GDB:305468; OMIM:600270
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A; Residues: 1-449 < TAK>
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T31069
T0110id-BMP-1 like protein 1 - California sea hare
t0110id-BMP-1 like protein 1 - California sea hare
t0110id-BMP-1 like protein 1 - California sea hare
t0.5pecies: Aplysia californica (California sea hare)
C.5pecies: Aplysia californica (California sea hare)
C.5cession: T31069
R.Liu, Q.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es
J. Neurosci. 17, 755-764, 1997
A.Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
A.Fitle: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
A.Fitle: A perliminary; translated from GB/BMBL/DDBJ

    sea urchin (Paracentrotus livid

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
                                                                                                                                                                                                                                                       149 LPPSALPLDLINNAITAFS----TLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   695 YPPD-----KNCVWHISAPKGHTLTVNFTHMDLE-WRGDECEL-----DFVRVTNVVG 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742 NKER-----LQGYCGFMAPPSITSLSNELRIEFRSDDTLQKTGFSMDYVADVDECASS 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           640 DHGCEHVCVNTLGSYECTCKIGYELHSDGKKCEKACGGYLDAPSGTISSPSF-----PDL 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RKSRVVDLNLLTEEVRLYSCTPRNFSVS--IREELKRTDTIFWPGCLL-----VKRCGGN 256
                                                                                                                                                                                                                  28 NGSIHSPRFPHTYPRNTVLVMRLVAVBENVWIQLIFDERFGLEDPEDDICKYDFVEVERP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-1070 -LIU>
A;Cross-references: EMBL,U57369; NID:g1899041; PID:g1899042; PIDN:AAC47485.1
C;Superfamily: dorsal-ventral patterning protein tolloid: settoin homelon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
871352
metalloproteinase (EC 3.4.24.-) 10 precursor, blastula - sea urchin (Paracer MiAlternate names: gene tolloid protein homolog C; Species: Paracentrotus lividus (common urchin) C; Date: 12-Feb-1999 #sequence revision 13-Mar-1998 #text_change 17-Mar-1999 C; Accession: $71352, A44801, $22060 C; Accession: $71352, A44801, $22060 E; Londond, G.; Ghiglione, C.; Lepage, T.; Gache, C. Eur. J. Biochem. 238, 744-751, 1996
F;158/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted F;444-445/Cleavage site: Arg-Ile (autolytic) #status predicted F;483,532,633/Active site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29 GSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL---TFDERFGLEDPEDDICKYDFVEVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 --EPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY------
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                                                                                                                                                                5;
                                                                                                     / Match B.3%; Score 143.5; DB 1; Length 686; Local Similarity 32.1%; Pred. No. 0.00025; les 34; Conservative 25; Mismatches 42; Indels 5
                                                                                                                                                                                                                                                                                                                                                      88 SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 133
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A,Title: Structure of the gene encoding the sea urchin blastula protease 10 (BP10), a r
A,Reference number: S71352, MUID:96300240; PMID:8706676
A,Accession: S71352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: A44880
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-7, 'S, 9-10, 'V', 12-28,'H', 30-72,'D', 74-77,'SK', 80-81,'I', 83-232,'R', 234-2:
9-571,'N', 573-584,'D', 586-595,'D', 597 <LEP>
A, Cross-references: EMBL:X56224; NID:g10928; PID:g10929
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                                                                                                                                                                                                                                                                         for residue 11 as Val, AAC for residue
                                                                                                                                                                                                                                                                                                                                                                                           οŧ
                                                                                                                      A; Molecule type: DNA
A; Residues: 1-597 < LHO>
A; Cross-references in EMBL.X65721; NID:e956534; PID:e46942
A; Experimental source: sperm
A; Experimental source: sperm
B; Note: the authors translated the codon GCT for residue 11 as Val, AAC for residue R; Lepage, T.; Ghiglione, C.; Gache, C.
Development 114, 147-163, 1992
A; Title: Spatial and temporal expression pattern during sea urchin embryogenesis of the patterning gene tolloid.
A; Reference number: A44880; MUID:92249197; PMID:1339338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 TTTI-STTTPVPTTTQATTDETVVGSCGGRFGGTQGRVATPNY--PNNYDNDLECVYVIE 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 VEV-----GRRVELDFIDFVLEDET--NCRMDSLSINLGDGIK------IDMKM 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             146 PSVLPPSALPLDLLNNAIT------AFSTLEDLI---RYLEPERWQLDLEDLYRPT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 WQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKR 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Introns: 30/3; 116/1; 184/3; 252/3; 370/3; 555/2
C; Superfamily: Clr/Cls repeat homology; astacin homology
C; Superfamily: Clr/Cls repeat homology; astacin homology
C; Keywords: hydrolase; metalloproteinase; zinc
F; 1-19/Domain: signal sequence #status predicted <SIG>
F; 20-59/Product: metalloproteinase 10, blastula #status predicted <MAT>
F; 339-446/Domain: Clr/Cls repeat homology <AST>
F; 3484-592/Domain: Clr/Cls repeat homology <CIRI>
F; 190, 194, 200/Binding site: zinc (His) #status predicted
F; 191/Active site: Glu #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.0%; Score 138.5; DB 2
Best Local Similarity 24.4%; Pred. No. 0.00056;
Matches 59; Conservative 44; Mismatches 92
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

November 25, 2003, 20:55:48; Search time 7.8869 Seconds (without alignments) 1896.117 Million cell updates/sec Run on:

US-09-852-209A-5 1734 1 GKFQPSSNKEQNGVQDPQHE.....DVALEHHEECDCVCRGSTGG 318

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence:

Scoring table:

127863 seqs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	xenobns	P98070 xenopus lae			P98063 mus musculu				035251 rattus norv	P97333 mus musculu		O57460 brachydanio	014786 homo sapien	P79795 gallus gall	Q15113 homo sapien	P25723 drosophila	043915 homo sapien		mus m	P42674 paracentrot		P98069 strongyloce				mus m		oryc	P97953 mus musculu		feli	O08859 mus musculu	908	
SUMMARIES	ID	NRPI	BMP1_XENLA		BMP1 HUMAN	BMP1 MOUSE	NRP1_RAT	NRP2 HUMAN	NRP2_RAT	VEGD_RAT	NRP1 MOUSE	NRP2_MOUSE	TLD BRARE	NRP1 HUMAN	NRP1_CHICK	PCO1_HUMAN	TLD DROME	VEGD HUMAN	MAS2_HUMAN	VEGD_MOUSE	BP10_PARLI	CRAR_MOUSE	BMPH_STRPU	C1R HUMAN	CRAR HUMAN	VEGC_HUMAN	PCO1_MOUSE	PCO1_RAT	PDGA_RABIT	VEGC_MOUSE		PDGB_FELCA	_9S8	TSG6_RABIT	
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P52585 orf virus (P01127 homo sapien P1369 xenopus lae P4264 xenopus lae P20033 mus musculu P2857 rattus norv P26617 cavia porce P01128 simian sarc P49765 homo sapien P15692 homo sapien P1692 homo sapien P52594 orf virus (
VECH ORFN7 PDGB_HUMAN PDGA_KENLA UVS2_KENLA PDGA_MOUSE PDGA_RAT VGGA_CAPPO TSIS_SMSAV VEGB_HUMAN VEGB_HUMAN PDGA_HUMAN VEGA_HUMAN	
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148 2241 2241 2214 204 207 207 2111 133	
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ALIGNMENTS

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MEROPS; M12.005;
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                                                                                                                                                                                                                                                                                                                                                                                                                       ----OFTEA--VSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWOLDLE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                   ECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFAPKMQEIV--LEFESFELEAD 197
                                                 Angiogenesis, Transmembrane, Glycoprotein, Neurone, Signal, Repeat;
Receptor; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.,

"Cloning and expression of cDNA encoding Xenopus laevis bone
morphogenetic protein-1 during early embryonic development.";

Gene 134:257-261(1993).

-!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
DIFFERENTIATION OF DEVELOPING ORGANS.

-!- DEVELOPMENTAL STAGE: BLASTULA, EARLY GASTRULA AND HATCHED
TADPOLES; LITTLE OR NO EXPERSSION IN MORULA AND LATE GASTRULA.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                 10.4%; Score 179.5; DB 1; Length 928; 31.6%; Pred. No. 1.5e-07; tive 29; Mismatches 73; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (BC 3.4.24.-) (BMP-1).
Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                          223 N-LINKED (GLCNAC, . .) (POT 344 N-LINKED (GLCNAC, . .) (POT 103416 MW; AF6B323B0A4C789D CRC64;
                                                                                        EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . . ) (P.
N-LINKED (GLCNAC. . . ) (F.
                                                                                                            CYTOPLASMIC (POTENTIAL).
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                                                                                                                                        F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                NEUROPILIN-1
                                                                                                                                                                                PROBABLE. PROBABLE.
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MEDLINE=94085787; PubMed=8262384;
 PROSITE; PS01285; FA58C_1; 2. PROSITE; PS01286; FA58C_2; 2. PROSITE; PS0022; FA58C_3; 2. PROSITE; PS00740; NAM 1; 1. PROSITE; PS50060; MAM_2; 1.
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                                                                                                                                                                                                                                                                                  928 AA;
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P98070;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00142; ZINC PROTEASE; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
PROSITE; PS001043; MYDROXYL; 1.
PROSITE; PS00002; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01186; EGF 2; 1.
Growth factor; Cytokine; Repeat, Bone; Cartilage; Hydrolase; Protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 NGSIHSPRPPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUB 1.
CUB 2.
EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
CUB 3.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)
(BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 -PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1B6980D716DC9B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.

ZINC (CATALYTIC) (BY SIM
BY SIMILARITY.
BY LINKED (GLCNAC. . . ) (CATALYTY.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.1%; Score 176; DB 1;
Best Local Similarity 43.3%; Pred. No. 2.1e-07;
Matches 45; Conservative 15; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
-1- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                                                                                                                                                                                                                               InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001851; CUB_domain.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001801; EGF_like.
InterPro; IPR006026; NZn_WIPeptdse.
InterPro; IPR006025; Zn_WIPeptdse.
Pfam; PF001400; Astacin; 1.
Pfam; PF001401; CUB; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80673 MW;
                                                                                                                                                                                                                                                                                                                       InterPro, IPR001506; Astacin.
                                                                                                                                                                                                                                  EMBL; 112249; AAA16313.1; -. PIR; JC2218; JC2218.
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO0480; ASTACIN.
SMART; SMO0042; CUB; 3.
SMART; SMO0179; EGF_CA; 1.
SMART; SMO235; ZNMC; 1.
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295
326
326
562
707 AA;
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protein-1.
DISULFID
DISULFID
DISULFID
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                         SEQUENCE
                                             Query Match
                                                     Best Local
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                                                             Matches
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                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=92315921; PubMed=1618141; MEDLINE=92315921; PubMed=1618141; Reynolds S.D., Angerer R.C.; Reynolds S.D., Angerer E.M., Palis J., Nasir A., Angerer R.C.; "Early mRNAs, spatially restricted along the animal-vegetal axis of sea urchin embryos, include one encoding a protein related to tolloid and BMP-1.";
                                                                                      Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Echinoida, Strongylocentrotidae,
                                                                                                                                                                                                                                                                                                                                                                                                               Development 114:769-786(1992).
-!- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS
OF THE BLASTULA.
                                                                                                                                                                                                                          -!- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATION PEPTIVE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPAN PROTEIN.
ARG/LYS-RICH (BASIC).
METALLOPROTEASE.
                                                                                                                                                                                                                                     AND HATCHING).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
--- SIMILARITY: Contains 1 EGF-like domain.
--- SIMILARITY: Contains 2 CUB domains.
                                            01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SPAN protein precursor (EC 3.4.24.-).
                             616 AA.
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CUB 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUB 1.
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InterPro; IPR000859; CUB domain.
InterPro; IPR006209; EGF_11ke.
InterPro; IPR006210; IEGF
                                                                                                                                                                                                                                                                                                                                                   EMBL; M84144; AAA30072.1; -. HSSP; P28825; 11AF.
                             STANDARD;
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616
616
616
8329
8329
1180
1191
1191
                                                                                                                  Strongylocentrotus.
NCBI_TaxID=7668;
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                             STRPU
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ACT SITE
METAL
METAL
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CHAIN
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           KESULT 3
SPAN_STRPU
                                      P98068
                               SPAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 TILQTTPPSTTTLQTTNPSTTTLQT-----TNPSTTTLQTTD--TPVIGSCGGTFV-G 509
                                                                                                                                                                                                                                                                                                        404
                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the human
                                                                                                                                                                                                                                                                                      GSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPS
                                                                                                                                                                                                                                                                                                                                                                   89 DGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPS--EPGFCIHYNIVMPQFTEAVSP
                                                                                                                                                                                                                                                                                                                                                                                                    405 INSIGERFCGN-TLPPVQISSSNQMMVSFTSD---PSITRRGFKATYVIII-QITTVFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 SVL---PPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          morphogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 RKSRVVDLNLLTEEVRLYSCTPRNFSVSIR-----EELKRTDTIF------W
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The C_proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BMP1 HUMAN STANDARD; PRT; 986 AA.
P13497; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38;
01-JJM-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (MTld)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M.J.,
                                                                                                                                                                                                63;
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"Three alternatively spliced variants of the gene coding for
bone morphogenetic protein-1 ";
J. Mol. Med. 76:141-146 (1998).
                                                                                                                                        DB 1; Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-89072730; PubMed-3201241;
Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters
Kriz R.W., Hewick R.M., Wang E.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-96209868; PubMed-8643539;
Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V.,
Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Novel regulators of bone formation: molecular clones and activities.";
                                                                                                                                                                                             93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7).
TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
397CD923FFB9EB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996)
                                                                                                                                        th 10.0%; Score 173.5; DB 1
| Similarity 27.0%; Pred. No. 2.9e-07, 70; Conservative 33; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM BMP1-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM BMP1-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE~Placenta;
MEDLINE=98160316; PubMed=9500680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 PGCLL------VKRCG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 DSLMINLGNGIKVGMKMCG 577
                                                                                   67902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 242:1528-1534(1988).
  299
305
319
616 AA;
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Astacin; 1.

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METAL
ACT SITE
METAL
METAL
DISULFID
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MEDLINE=95096114; PubMed=7798260;
Takahara K., Lyons G.E., Greenspan D.S.;
The morphogenetic protein-1 and a mammalian tolloid homologue (mrId)
Tare encoded by alternatively spliced transcripts which are
differentially expressed in some tissues.";

U. Biol. Chem. 269:32572-32578 (1994).

NEDLINE=21336528; PubMed=11283002;
MEDLINE=21336528; PubMed=11283002;
MEDLINE=21336528; PubMed=11283002;
MEDLINE=21336528; PubMed=11283002;
Tarigue-Antear L., Barker C., Kadler K.E.;
Tortein-1 important for procollagen C-proteinase activity.";
U. Biol. Chem. 276:26237-2642(2001).
U. Biol. Chem. 276:26237-2642(2001).
AND II. INDUCES CARTILAGE AND BONE FORMATION.
AND II. INDUCES CARTILAGE AND BONE FORMATION.
AND II. INDUCES CARTILAGE AND BONE FORMATION.
AND II. TAPPE I and II procollagens and at Arg-|-Asp in type I and II procollagens and at Arg-|-Asp in type I and II procollagens and at Arg-|-Asp in type
                                                                                                                                                                                                                                                            -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
ENDOPEPTIDASE ENHANCER PROTEIN.
-!- ALTERRATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                         Name=BMP1-4;
IsoId=P13497-3; Sequence=VSP_005463; VSP_005464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P13497-4; Sequence=VSP_005465, VSP_005466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P13497-5; Sequence=VSP_005467, VSP_005468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOId=P13497-6; Sequence=VSP 005469, VSP_005470; -1 TISSUE SPECIFICITY: Ubiquitcous.
-1 SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
-1 SIMILARITY: Contains 2 EGF-like domains.
-1 SIMILARITY: Contains 5 CUB domains.
                                                                                                                                                                                                                                                                                                                                                                             IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P13497-7; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                  IsoId=P13497-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                   Name=BMP1-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=BMP1-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=BMP1-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=BMP1-6;
                                                                                                                                                                                                                                                                                                                                                                                               Name=BMP1-2;
                                                                                                                                                                                                                                                                                                                                     Name=BMP1-3
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DKDECSKDNGGCQQDCVNTPGSYECCR -> EKRPALQPP
RGRPHQLKFRVQKRNRTPQ (in isoform BMP1-1).
/FIId=VSP_005461.
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Misaing (In isoform BMP1-6).
/FTId=VSP_005468.
DXDECSKDNGGCQQDCVNTFGSYECQCRSGFVLHDNKHDCK
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IVPKYEVNGVKPPIGQR -> VLHSSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUB 3.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 005465.
Missing (In isoform BMP1-5).
/FTId=VSP 005466.
DKDECSKDNGGCQQD -> GGELFGLIGHPPRRP (in
                                                                   PERMI, PF00008; MGF; 2.

PRINTE; PR00480; ASTACIN.

SMART; SM000179; BGF_CA; 2.

SMART; SM00179; BGF_CA; 2.

SMART; SM00179; BGF_CA; 2.

SMART; SM00179; BGF_CA; 2.

RMART; SM00179; BGF_CA; 2.

PROSITE; PS001180; CUB; 5.

PROSITE; PS001180; CUB; 5.

PROSITE; PS001180; CUB; 5.

PROSITE; PS001180; CUB; 5.

PROSITE; PS001180; CUB; 2.

PROSITE; PS001180; EGF_Z; 2.

R PROSITE; PS001180; EGF_Z; 2.

R PROSITE; PS001187; EGF_Z; 2.

R PROSITE; PS001187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL) .
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DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (in
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SIMILARITY)
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Missing (in isoform BMP1-4).
/FIId=VSP_005464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (In isoform BMP1-1).
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BY SIM
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(BY
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ZINC (CATALYTIC)
ZINC (CATALYTIC)
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Pfam; PF01400; Astacin;
Pfam; PF00431; CUB; 5.
Pfam; PF00008; BGF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986
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us-09-852-209a-5.rsp

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39.48;
EMBL; L24755; AAA37306.1;
                                                                                                                                                                                                                                                                                                 PR00480; ASTACIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Zymogen
                    PIR; 149540; 149540.
HSSP; P00736; 1APQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      991 AA;
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                                                       MEROPS; M12.005; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
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DISULFID
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CARBOHYD
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DOMAIN
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SOLITIES SOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                             599 NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEG-----NDVCKYDFVEVRS 653
                                                                                                                                                                                                                                                                                                                                        28 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 86
                    COFACTOR: Binds 1 zinc ion per subunit (By similarity).
ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDOPEPPITASE ENHANCER PROTEIN.
TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDUUM
AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING
  EAGCDHKVTSTSGTITSPNWPDKYPSKKECTWAISSTPGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, III AND II. INDUCES CARTILAGE AND BONE FORMATION.
-I- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at Ala-|-Asp in type I and II procollagens and at Arg-|-Asp in type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEMBERNOUS AND ENDOCHONDRAL BONE, SUBMUCOSA OF INTESTINE, DERMIS OF SKIN AND THE MESENCHYME OF SPLEEN AND LUNG.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
-!- SIMILARITY: CONTAINS 5 EGF-like domains.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukagawa M., Noboru S., Hogan B.L.M., Jones C.M.; "Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1), which is related to the Drosophila dorsoventral gene tolloid and encodes a putative astacin metalloendopeptidase.";

Dev. Biol. 163:175-183(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMD-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (#Tld)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                           87 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 133
                                                                                                                                                                                                                                                         Length 986;
                                                                                                                                                                                                                                                                                                 39; Indels
                                                                                            L (in isoform BMP1-7).
/FTId=VSP_005469.
Missing (in isoform BMP1-7)
/FTId=VSP_005470.
                                                                                                                                                                         -> N (IN REF. 4).
-> S (IN REF. 4).
F89201913AC3CBEA CRC64;
                                                                                                                                                                                                                                                         Score 169; DB 1;
Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          991 AA
                                                                                                                                                                                                                                                                                               17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Embryo;
MEDLINE=94229342; PubMed=8174772;
                                                                                                                                                                               Ω
                                                                                                                                                                                                                      111248 MW;
                                                                                                                                                                                                                                                           9.7%;
                                                                                                                                                                                                                                                                                                   43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Mouse)
                                                                                                                                                                                                    934 9
986 AA;
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BMP1 MOUSE
P98063;
                                                                                                                                                                                                    CONFLICT
                                                                                                                                            VARSPLIC
                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KESULT 5
BMP1_MOUSE
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28 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 86
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CUB 3.

EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).

CUB 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY SIMILARITY)
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(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00042; CUB; 5.
SMART; SM00042; CUB; 5.
SMART; SM00235, ZMG; 1.
PROSITE; PS00142; ZINC PROTEASE; 1.
PROSITE; PS00180; CUB; 5.
PROSITE; PS00101 ASK HYDROXYL; 2.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF 2; 2.
PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
BONE MORPHOGENETIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      =
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604 N-LINKED (GLCNAC. . .)
111607 MW; 68A1847783A0BB9E CR(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
N-LINKED (GLCNAC. .
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N-LINKED (GLCNAC.
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ZINC (CATALYTIC)
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MGD; MGI:88176; Bmpl.
InterPro; IPR001505; Astacin.
InterPro; IPR001505; Ast Mydroxyl.
InterPro; IPR001895; CUB domain.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR00209; EGF_Iike.
InterPro; IPR005026; NGP_Iike.
InterPro; IPR006025; Zn_WTpeptdse.
InterPro; IPR006025; Zn_WTpeptdse.
Pfam; PF00400, Astacin; 1.
Pfam; PP00008; EGF; 2.
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659 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705

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Cardioval is a semaphorin III receptor.";

Ginty D.D.;

"Neuropilin is a semaphorin III receptor.";

Cell 90:753-762(1997).

Cell 90:753-762(1997).

CARDIOVASCULAR SYSTEM, IN ANGIOGRNESIS, IN THE PORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATE THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT STORE THE OFFICE ISOPREM OF VEGF AND VEGF-B. COEXPRESSION WITH KOR RESULTS. IN THE VEGF-165 BINDS TO SEMAPHORINS. OF THE VEGF-165 BINDS TO VEGF-B. COEXPRESSION WITH KOR RESULTS. IN TROPERASED CHEMOTAXIS.

C.I. SUBCELLULAR LOCATION: Type I membrane protein.

C.I. SUBCELLULAR COATION: Type I membrane protein.

C.I. SIMILARITY: Contains 2 CUB domains.

C.I. SIMILARITY: Contains 2 FS/B type C domains.

C.I. SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Neurone; Signal; Repeat;
                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                        Kolodkin A.L., Levengood D.V., Rowe B.G., Tai Y.-T., Giger R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL) .
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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922
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INTERPRO; IPRO00859, CUB domain.
INTERPRO; IPRO00421; FASE C.
INTERPRO; IPRO00998, MAM_Gomain.
PETAN, PETO0431; CUB; 2.
PETAN, PETO0629, MAM; 1.
PRINTS; PRO0020; MAMDOMAIN.
SWART; SW00231; FASEC; 2.
SWART; SW00231; FASEC; 2.
SWART; SW00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FASEC_1; 2.
PROSITE; PS01285; FASEC_2; 2.
PROSITE; PS01022; FASEC_3; 2.
PROSITE; PS01022; FASEC_3; 2.
PROSITE; PS00022; FASEC_3; 2.
PROSITE; PS50022; FASEC_3; 2.
PROSITE; PS50022; FASEC_3; 2.
PROSITE; PS500440; MAM_1; 1.
PROSITE; PS500440; MAM_1; 1.
                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF016296; AAC53337.1; -.
HSSP; P12259; 1CZT.
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STANDARD;
                                                                                                                                      Rattus norvegicus (Rat).
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880
922
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22
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NRP1 RAT
Q9QWJ9;
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MEDLINE=20309748; PubMed=10748121;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
growth factor-z. but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";
J. Blod. Chem. 275:18040-18045(2000).
-: FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
-: SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDBRFGLEDPEDDICKYDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
MEDLINE=97470888; PubMed=9331348;
Chen H., Chedoral A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
Chen H., Chedoral A., The Select of Select o
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRP2 HUMAN STANDARD; PRT; 931 AA.
060466; 014820; 014821;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soker S., Takashima S., Mao H. O., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
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                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                             9.4%; Score 163.5; DB 1; Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels
                                                                                                                                                                                                                                                                                                                                                             103082 MW; CC6F82AD098B0F2E CRC64;
                                                                                                                                                                                                                                                                                                                       (GLCNAC. . .)
(GLCNAC. . .)
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BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                             υU
                                           F5/8 TYPE (F5/8 TYPE (
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MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                                                                                                                                                                                                                                                                                          36.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
receptor 2).
NRP2 OR VEGF165R2.
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    DOMAIN
DOMAIN
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SEQUENCE FROM N.A.
   809
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ID NRP2 RAT
AC 035276;
                       CONFLICT
   VARSPLIC
                                                                              Matches
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DR EMBL; AF022860; AAC51788.1; -.

DR EMBL; AF022860; AAC51788.1; -.

DR EMBL; AF016098; AAC12922.1; -.

DR RISE; P12259; 1CZT.

DR RISE; P12259; 1CZT.

DR GO:00005021; F:receptor activity; TAS.

GO:00004812; F:receptor activity; TAS.

GO; GO:00005021; F:vascular endothelial growth factor receptor. .; TAS.

DR GO; GO:0000411; F:vascular endothelial growth factor receptor. .; TAS.

DR GO; GO:0000411; F:vascular endothelial growth factor receptor. .; TAS.

DR GO; GO:0000421; F:vascular endothelial growth factor receptor. .; TAS.

DR GO; GO:0000421; FASE C.

DR InterPro; IPR000998; MAM_domain.

Pfam; PF000431; CUB; 2.

DR Pfam; PF00020; MAMDOMAIN.

DR SMART; SM00042; CUB; 2.

DR SMART; SM00137; MAM; 1.

DR SMART; SM00137; MAM; 1.

DR ROSITE; PS01285; FASEC_1; 2.

DR PROSITE; PS01285; FASEC_1; 2.

DR PROSITE; PS01285; FASEC_1; 2.

DR PROSITE; PS01285; FASEC_2; 2.

DR PROSITE; PS01086; MAM_2; 1.

PROSITE; PS00000; MAM_2; 1.

PROSITE; PS00000; MAM_2; 1.

PROSITE; PS00000; MAM_2; 1.

PROSITE; PS00000; MAM_2; 1.

PM Transmembrands Glycoprotein; Neurone; Signal; Receptor;

WM Transmembrands Glycoprotein; Neurone; Signal; Receptor;
                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR. SUBCELLULAR LOCATION: Type I membrane protein. ALTERNAȚIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                Isold=060462-3; Sequence=VSP_004341;
-:- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-:- SIMILARITY: Contains 2 CUB domains.
-:- SIMILARITY: Contains 2 F5/8 type C domains.
-:- SIMILARITY: Contains 1 MAM domain.
                                    Event=Alternative splicing; Named isoforms=3;
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
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CUB 2.
F5/8 TYPE C 1
F5/8 TYPE C 2
                                                                               IsoId=060462-2; Sequence=VSP_004342;
                                                          IsoId=060462-1; Sequence=Displayed;
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864
931
1442
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8022
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152
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629
839
813
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SIGNAL 1 20
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21
21
885
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277
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83
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1152
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                                                 Name=A22;
                                                                      Name=A0;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBL_TaxID=10116;
                                                                                                                                                               Gaps
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STEAIN=Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
                                                                                                                                                             7;
                                                                                                          ch 9.4%; Score 163.5; DB 1; Length 931; 1 Similarity 32.3%; Pred. No. 3.6e-06; 43; Conservative 19; Mismatches 64; Indels 7;
                   /FTIG=VSP 004342.

102 E -> K (IN REF. 1).

104830 MW; 270CBAE69A0A797C CRC64;
Missing (in isoform A0).
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InterPro; IPR000421; FAS8 C.
InterPro; IPR000998; MAM_domain.
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SMART; SM00042; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                123 FPSEPGFCIHYNI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AROGAGFSLRYEI 141
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                                                                                                                    Query Match
Best Local Similarity
                                                602 (
931 AA;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 PHFEIEKHD---CKYDFIEIRDGDSESADLLGKHCGN-IAPPIISSGSVLYIKFTSD-Y 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Sprague-Dawley;
Yamada Y., Hirata Y., Nezu J., Shimane M.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Growth factor active in anglogenesis, lymphanglogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Vascular endothelial growth factor D precursor (VEGF-D) (c-fos induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FSGHKVRS-QODPPCGGRLNSKDAGYITSPGYPQDYPSHQNCEWVVYAPEPNQKIVLNFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERFGLEDPEDDICKYDFVEVE--EPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                5 FSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                D (GLCNAC. ..) (FOURTIAL).

D (GLCNAC. ..) (POTENTIAL).

ED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                          Neurone; Signal; Repeat; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                               Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                         60; Indels
                                                                                                                                                                                                                                                                                                                                                                 103896 MW; 3BF62903F644851C CRC64;
                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                      F5/8 TYPE C 1.
F5/8 TYPE C 2.
MAN.
BY SIMILARITY.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                9.4%; Score 163; DB 1;
33.8%; Pred. No. 3.9e-06;
iive 20; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                               N-LINKED
                                                                                                                                                                    CGB 1.
SWART; SM00231; FA58C; 2.
SWART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_2; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS50022; FA58C_3; 2.
PROSITE; PS50060; MAM_2; 1.
Transmembrane; Glycoprotein; Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 FPSEPGFCIHYNI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARQGAĞFSLRYEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth factor) (FIGF) FIGF OR VEGFD.
                                                                                                                                                                                                                                                                                                                                                               834
925 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                           45;
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                                                                                                                                                                                                                                                                       DISULFID
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TRANSMEM
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DOMAIN
DOMAIN
DOMAIN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 GECIHYNIVMPQFTEAVSPSVLPPSALPLDLLMNAITAFSTLEDLIRYLEPERWQLDLED 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-KRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCV---PSKVTKKYHEVLQLRPKTGVR 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68
            -:- SUBUNIT: Homodimer; non-covalent and antiparallel (By similarity).
-:- SUBCELLULAR LOCATION: Secreted (By similarity)
-:- FWH: Undergoes a complex proteolyric maturation which generates a variety of processed secreted forms with increased activity toward vegrey of processed secreted forms with increased activity toward vegrey of secreted forms of the increased activity toward vegrey of substitute bods before secretion. The fully processed vegre- is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).
-:- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 LWRCRLKLKSLANVDSRSTSHRSTRFAATFYDTETLKVIDEEWORTOCSPRETCVEVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 IGKTINTFFKPPCVNVFRCGG---CC--NEESVMCMNTST$YISKQLFEISV--PLTSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GFSIEHRAVKDVSLERSSRSVLERS-----BQQIRAASTLEELLQVAHSEDWK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYRPTWQLLGKAFVFGRKSR--------VVDLNLLTEEVRLYSCTPRNFSVSIREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00141; rune, ...
PROSITE, PS00249; PDGF_1; 1.
PROSITE, PS50278; PDGF_1; 1.
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
Cleavage on pair of basic residues; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
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N-LINKED (GLCNAC. .) (POTENTIAL)
N-LINKED (GLCNAC. .) (POTENTIAL)
1261AFA373596C00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (INCOMPLETE).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80; Indels
activates VEGFR-3 (Flt4) receptor (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 162.5; DB 1
30.0%; Pred. No. 1.2e-06;
iive 23; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APPROXIMATE)
                                                                                                                                                                                                                                                                                                                              EMBL; AF014827; AAB66E57.1; -...
HSSP; P15692; 1VPP.
InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF03128; CXCXC; 1...
Pfam; PF0341; PDGF; 1...
ProDom; PD001629; PD_growth_factor; 1...
SWART; SM00141; PDGF; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 GLHKSLTDVALEHHEECDCVCRG 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PELVPVKIANHTGCKCLPTG 200
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292
326 AA;
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94
211
227
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DISULFID
DISULFID
DISULFID
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Name=B0;
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        DISULFID
                                                     DISULFID
                                                                          CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                              DISULFID
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                                            DISULFID
                                                                                                                                                                      Local
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NRP2 MOUSE
                                                                                                                                                                      Best Loc
Matches
844444444
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                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIINE=96383149; PubMed=8748368;

MEDIINE=96383149; PubMed=8748368;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Tourophiln, in the mouse nervous system.";

J. Neurobiol. 29:1-17(1996).

CARDIOMASCULAR SYSTEM, IN ANGIOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT IN MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS. IT STOREASED VEGF-165 BINDING TO NEW AS WELL AS INCREASED CHEMOTAXIS.

IN MAY REGULATE VEGF-1 INDUCED ANGIOGENESIS (BY SIMILARITY).

CHORAGO VEGF-165 BINDING TO NEW AS WELL AS INCREASED CHEMOTAXIS.

THE STRUILARITY: SELONGS TO THE NEWROPTILIN FAMILY.

CHORAGO SYSTEM.

SIMILARITY: Contains 2 CUB domains.

CHORAGO SYSTEM.

SIMILARITY: Contains 2 FS/8 type C domains.
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BKBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibe.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Neurone; Signal; Repeat;
                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL)
                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-1 precursor (A5 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CUB 2.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
             923 AA.
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:106206; Nrp.
InterPro; IPR000989; CUB domain.
InterPro; IPR000989; MAM Gomain.
Pfam; PR0041; CUB; 2.
Pfam; PF00441; CUB; 2.
Pfam; PF00764; F5 F8 Lype_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0020; MAMDOMAIN.
SMART; SM00042; CUB; 2.
SMART; SM0137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FAS8C 1; 2.
PROSITE; PS01285; FAS8C 2; 2.
PROSITE; PS0022; FAS8C 2; 2.
PROSITE; PS00740; MAM 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis; Transmembrane; Receptor. 1 21 81GNAL 1 22 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D50086; BAA08789.1; -- HSSP; P12259; 1CZT.
             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
923
856
879
923
141
141
265
583
                                                                                         Mus musculus (Mouse)
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22
22
8857
880
277
431
                                                                               OR NRP.
             NRP1 MOUSE
P97333;
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TRANSMEM
DOMAIN
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DOMAIN
DOMAIN
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4
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-!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES, INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
-!- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BALB/c;
MEDLINE=97470888; PubMed=9331348;
MEDLINE=97470888; PubMed=9331348;
Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
Chen H., Chedotal A., He S.-G., Goodman C.S., Tessier-Lavigne M.;
"Neuropilin-2, a novel member of the neuropilin family, is a high
affinity receptor for the semaphorins Sema B and Sema IV but not Sema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuron 19:547-559(1997).
-!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORING 3C, 3F, VEGF-165
-!- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORING OF PGF.
-!- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
-!- SUBCELLINIAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 EVIDGENEGGRLMGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRP2 MOUSE STANDARD; PRT; 931 AA.
035375; 035374; 035376; 035377; 035378;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
18-EBS-2003 (Rel. 41, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                424 BY SIMILARITY.

583 BY SIMILARITY.

150 N-LINKED (GLCNAC. . .) (POTENTIAL).

261 N-LINKED (GLCNAC. . .) (POTENTIAL).

300 N-LINKED (GLCNAC. . .) (POTENTIAL).

522 N-LINKED (GLCNAC. . .) (POTENTIAL).

423 N-LINKED (GLCNAC. . .) (POTENTIAL).

103020 MW; 0644B8Al70796808 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 160.5; DB 1
36.5%; Pred. No. 6.4e-06;
Live 16; Mismatches 50
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Similarity 42; Conserva
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NRP2.
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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LTIKLEQERGSHC (in isoform B0).
/FTId=VSP_004346.
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EXTRACELLULAR (POTENTIAL)
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DEVELOPMENTALLY REGULATED.
--- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
--- SIMILARITY: Contains 2 CUB domains.
--- SIMILARITY: Contains 2 F5/8 type C domains.
--- SIMILARITY: Contains 1 MAM domain.
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F5/8 TYPE C 2.
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InterPro; IPR000859; CUB domain.
InterPro; IPR000859; CUB domain.
Pfam; PP00431; FASB C.
Ffam; PP00431; CUB; 2.
Pfam; PP00754; FS Pg type_C; 2.
Pfam; PP00629; MAM; 1.
PRINTS; PR000720; MAMDOMAIN.
SMART; SM0042; CUB; 2.
SWART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01286; FASBC, 2.
PROSITE; PS01286; PASBC, 2; 2.
PROSITE; PS01029; PASBC, 2; 2.
PROSITE; PS01029; PASBC, 2; 2.
PROSITE; PS01029; PASBC, 2; 2.
                                                                                                                                                                                                                                       EMBL, AF022856; AAC53379.1; --
EMBL, AF022855; AAC53377.1; --
EMBL, AF022855; AAC53378.1; --
EMBL, AF022857; AAC53380.1; --
EMBL, AF022868; AAC53381.1; --
EMBL, AF022861; AAC53381.1; --
EMBL, AF022861; AAC53382.1; --
HSSP; P12259; 1CZT.
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                                                                         GILPPOTERTYDTVPVQPIPAYWYYVWAAGGAVLVLASVVL
ALVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEPLTI
KLEQERGSHC (in isoform B5).
Frieder (in isoform B5).
Frieder (in REF. 1; AAC53380/AAC53381).
                       EKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCTCSYS
GLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA -> G
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-1- TISSUE SPECIFICITY: During gastrulation, accumulates around the closing blastopore with greater expression ventrally. At the animal pole, expressed in the ectoderm flanking the anterior neural plate. At the 10-somite stage, expressed in the developing tailbud and cranial neural crest. At the 20-somite stage, also expressed in the hematopoietic system.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
-1- SIMILARITY: Contains 5 CUB domains.
VDIPETHGGEGYEDEIDDEYEGDWSNSSSSTSGAGDPSSGK
                                                                                                                                                                                                                                                                                                                                                                                          5 FSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOLLOID OR TLD OR MEN.
Brachydanio rerio (Zebrafish) (Danio rerio).
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Development 126.3119-3130(1999).
-!- FUNCTION: Required for paterning ventral tissues of the tail. M
-!- FUNCTION: Required for paterning ventral tissues of the end of
increase bone morphogenetic protein (BMP) activity at the end of
gastrulation by proteclytic cleavage of chordin and release of B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Gastrula;
MEDLINE-98057457; PubMed-9395394;
Bader P., Rastegar S., Fischer N., Straehle U.;
"Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid.";
Science 278:1937-1940(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-)
(Mini fin protein).
                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                  DB 1; Length 931;
                                                                                                                                                                                                                                                                                                                                        65; Indels
                                                                                                                                                                                                                       104558 MW; 76F2443F411D2F63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                               Score 159.5; DB 1
Pred. No. 7.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1022 AA
                                                                                                                                                                                                                                                                                                                                          17; Mismatches
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                                                                                                                                                                                                                                                                                  9.2%;
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                                                                                                                                                                                                                                                                                                                                             44; Conservative
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Best Local 6
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SMART; SMO01042; CUB; 5.
SMART; SMO0104; EGE_CA; 2.
SMART; SMO0104; EGE_CA; 2.
SMART; SMO0104; EGE_CA; 1.
PROSITE; PSO0101; ASX_HYDROXYL; 2.
PROSITE; PSO1186; EGE_1; FALSE_NEG.
PROSITE; PSO1187; EGF_2; 2.
PROSITE; PSO1187; EGF_CA; 2.
PROSITE; PSO1147; ZINC_PROTEASE; 1.
Developmental protein; Hydrolase; Protease; Metalloprotease; Zinc; Metal-binding; Calcium; EGF-like domain; Repeat; Signal; Glycoprotein;
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(BY SIMILARITY)
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BY SIMILARITY.
ZINC (CATALYTIC) (B)
ZINC (CATALYTIC) (B)
BY SIMILARITY.
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HSSP; P35555; 1EMN.
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                                                                     28 NGSIHSPRFPHTYPRNTVLVMRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE-
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                            Gaps
                                                                                                                                                                                                        NRP1_HUMAN STANDARD; PRT; 923 AA.
014786; 060461;
30-MAY-2000 (Rel. 39, Created)
16-OCT-2011 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soker S., Takashima S., Miao H.-O., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                           "Neuropilin is a receptor for the axonal chemorepellent semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to inhibit its binding to cells. It may also induce apoptosis by sequestering VEGF-165. May bind as well various members of the
                                                                                                                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                            8
                                                                                                                        87 -PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 133
 Length 1022;
                            38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity.";
Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000)
9.2%; Score 159; DB 1;
39.8%; Pred. No. 9.7e-06;
tive 19; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Prostatic adenocarcinoma;
MEDLINE=20183929; PubMed=10688880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION.
MEDLINE=20309748; PubMed=10748121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=97433084; Pubmed=9288753;
                                                                                                                                                                                                                                                                                                                                                                                                              He Z., Tessier-Lavigne M.;
                            Conservative
                                                                                                                                                                                                                                                                                         receptor).
NRP1 OR NRP OR VEGF165R.
                                                                                                                                                                                                                                                                                                                                                                                                                                         III.";
Cell 90:739-751(1997)
                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
               Local Similarity
hes 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity."
    Query Match
                                                                                                                                                                            RESULT 13
NRP1_HUMAN
                  Best Loca
Matches
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STANDARD;
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173
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749 7
855 8
923 AA;
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                                                                                                            645
                                                                                                                                                                                                                                                                                                                                                                                             NRP1 OR NRP.
                                                                                                                                                                                                                                                                                                                                  CHICK
                                                                                                                                                                                                                                                                                88
                  DISULFID
                                                                                                                                       CONFLICT
                                                                                                                                                                               Query Match
                                                                                        VARSPLIC
                                                                                                            VARSPLIC
                                                                                                                             CONFLICT
                                                                                                                                                            SEQUENCE
          DISULFID
                                      CARBOHYD
                                                 CARBOHYD
                                                          CARBOHYD
                                                                    CARBOHYD
                                                                              CARBOHYD
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P79795;
                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                              RESULT 14
NRP1 CHICK
                                                                                                                                                                                                    Matches
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Name=2; Synonyms=Soluble, SNRP1; 900439, VSP 004340;

Isold=014786-2; Sequence=VSP 004339, VSP 004340;

Isold=014786-2; Sequence=VSP 004340;

In the developing embryo it is found in the nervous system. In adult tissues, it is predominantly in the nervous system. In adult tissues, it is highly expressed in heart and placenta; moderately in lung, liver, skeletal muscle, kidney and pancreas; and low in adult brain.

Isolorm 2 is found in liver hepatocytes, kidney distal and proximal tubules.

Isolorm 2 is found in liver hepatocytes, kidney distal and proximal tubules.

Isolorm 2 to THE NEUROPLIN FAMILY.

                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    semaphorin family. Its expression has an averse effect on blood vessel number and integrity. SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                        ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=1; Synonyms=Membrane-bound;
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F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   999
                                                                                                                                                                                                                                                                                                              EMBL, AF018956; AAC51759.1; -.
EMBL; AF016050; AAC12921.1; -.
EMBL; AF145712; AAF44344.1; -.
PDB; 1KEX; 28-JAN-03.
Genew; HGNC:8004; NRP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWART; SM00042; CUB; 2.
SMART; SM00213; FASEC; 2.
SMART; SM00213; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FASEC_1; 2.
PROSITE; PS01286; FASEC_2; 2.
PROSITE; PS01286; FASEC_3; 2.
PROSITE; PS50022; FASEC_3; 2.
PROSITE; PS50060; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
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TRANSMEM
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DISULFID
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Dev. Biol. 170:207-222(1995).

-I- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAHORINS (BY
SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           varius garius (unioken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 135
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
FFP -> GIK (in isoform 2).
/FTIG=VSP 004339.
Missing (in isoform 2).
/FTIG=VSP_004340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 9.1%; Score 158.5; DB 1; Length 1 Similarity 35.7%; Pred. No. 9.5e-06; 41; Conservative 18; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                           26 K -> E (IN REF. 1).
749 D -> H (IN REF. 2).
855 E -> D (IN REF. 2).
103120 MW; ADEADC4A849E5D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=White leghorn, TISSUE=Embryonic brain; MEDLINE=95324761; PubMed=7601310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-ROV-1997 (Rel. 35, Last sequence update)
Neuropilin-1 precursor (A5 protein)
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PROBABLE.
BY SIMILARITY.
BY SIMILARITY.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 EVIDGDNAEGRLWGKYCGK-IAPPPLVSSGPYLFIKFVSD-YETHGAGFSIRXEVFKRGP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVM--P 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 IKILSPGYLTSPGYPGSYHPSQKCEWLIQAPEPYQRIMINFNPHFDLEDRD---CKYDYV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 ECSRNFTSSSGMIKSPGFPEKYPNSLECTVIIFAPKWSEILLEFESFE-----LEPD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 Q----FIEAVSPSVLP--PSALPLDL-----LINNAITAFSTLEDLIRYLEPE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCOL HUMAN STANDARD; PRT; 449 AA.
Q1513, 014550;
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2000 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COOH-terminal proteinase enhancer) (Type I procollagen COCH-terminal) proteinase enhancer)
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                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0020; MAMDOMAIN.
SMART; SM00042; CUB; 2.
SMART; SM00131; PASSC; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FASSC 1; 2.
PROSITE; PS0022; FASSC 2; 2.
PROSITE; PS00740; MAM 1; 1.
PROSITE; PS00740; MAM 1; 1.
PROSITE; PS0060; MAM 2; 1.
PROSITE; PS0060; MAM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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SIMILARITY.
DD2EEGD6F0CBB68C CRC64;
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EXTRACELLULAR (POTENTIAL)
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CUB 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.1%; Score 157; DB 1; 29.4%; Pred. No. 1.3e-05;
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F5/8 TYPE C 1.
F5/8 TYPE C 2.
MAM.
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                                                                                                                                                                                 InterPro; IPR000859; CUB domain.
InterPro; IPR000421; FA58 C.
InterPro; IPR000998; MAM_domain.
Fam; PF00431; CUB; 2.
Pfam; PF00754; FS F8 type_C; 2.
Pfam; PF00629; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102480 MW;
                                                                                                                                     EMBL; D45416; BAA08256.1; -. HSSP; P12259; 1CZT.
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52;
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MICHONING R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Alterubberg R.L., Feingold E.A., Wagner L., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Blard N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Branstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Wadran P.J., McKernan K.J., Mallek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

"Manner A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                      MEDLINE=95014462; PubMed=7523404;
Takahara K., Kessler E., Biniaminov L., Brusel M., Eddy R.L.,
Jani-Sait S., Shows T.B., Greenspan D.S.;
"Type I procollagen COGH-terminal proteinase enhancer protein:
identification, primary structure, and chromosomal localization of the
cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26285(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99134301; PubMed=9933570; Scott I.C., Clark T.C., Takahara K., Hoffman G.G., Greenspan D.S.; Scott I.C., Clark T.C., Takahara K., Hoffman G.G., Greensiaation and expression patterns of the human and mouse genes for the type I procollagen COOH-terminal proteinase
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                Unpublished observations (FEB-2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reveals 17 genes.";
Genome Res. 8:1060-1073(1998).
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Genomics 55:229-234(1999).
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                      NCBI_TaxID=9606;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAKE 280
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-!- FUNCTION: BINDS TO THE COCH-TERMINAL PROPEPTIDE OF TYPE I PROCOLLAGEN AND ENHANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
-!- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN METALLOPROTEINASE INHIBITORY ACTIVITY.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PTM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
-!- SIMILARITY: Contains 2 CUB domains.
-!- SIMILARITY: Contains 1 NTR domain.
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CLEAVAGE.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
3D88430158648796 CRC64;
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PROCOLLAGEN C-PROTEINASE ENHANCER
PROCTEIN.
CUB 1.
CUB 2.
NTR.
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Best Local Similarity 33.8%; Pred. No. 9.4e-06;
Matches 48; Conservative 22; Mismatches 50; Indels 2
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Pfam; PF00411; CUB; 2.
Pfam; PF01759; NTR; 1.
SMART; SM00643; C345C; 1.
SMART; SM00042; CUB; 2.
PROSITE; PS01180; CUB; 2.
Glycoprotein; Repeat; Signal.
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completed: November 25, 2003, 21:02:51 ne : 8.8869 secs

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November 25, 2003, 20:58:59; Search time 28.0774 Seconds (without alignments) 2922.663 Million cell updates/sec
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1734
1 GKRQFSSNKEQNGVQDPQHE.....DVALEHHEECDCVCRGSTGG 318
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q9nral homo sapien	Ogdy71 mus musculu	Q8ci19 mus musculu	Q9eqx6 rattus norv	Q9jhv8 mus musculu	Q9i946 gallus gall	Q8k429 rattus norv	Q9gzp0 homo sapien	Q9bwv5 homo sapien	Q9eqt1 rattus norv	Q925i7 mus musculu	Q8k2l3 mus musculu	Q8qfx6 brachydanio	Q8axp1 brachydanio	O57658 gallus gall
SUMMARIES	Q	29NRA1	090Y71	QBCI19	ОЭБОХ6	болнув	Q9I946	Q8K429	D9GZP0	29BWV5	Q9EQT1	092517	Q8K2L3	QBQFX6	Q8AXP1	057658
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	% Query Match Length DB	345	3.45 2.45	345	345	345	345	258	370	364	370	370	261	923	923	691
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Q99jm4 mus musculu	Q91925 xenopus lae	O60494 homo sapien	Obwym6 mus musculu	O57381 xenopus lae	Q9uq00 homo sapien	Q9y617 homo sapien	Q9z135 rattus norv	070244 rattus norv	Osppzo mus musculu	O8qzy7 mus musculu	homo	homo	pomod.	Q9h2d4 homo sapien	Q9h2e3 homo sapien	Q9qx38 rattus norv	Q8ji28 xenopus lae	Q9tu53 canis famil	Q96i90 homo sapien	Q96ih5 homo sapien	Q9h2el homo sapien	Q8uvr0 gallus gall	Q8uvq9 gallus gall	Q9der7 gallus gall	Q9ukz9 homo sapien	O57382 xenopus lae	Q91ze4 rattus norv	Q9brh3 homo sapien
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10.4	10.1	10.0	6	9.9	6.	6.6	9.7	9.7	9.5	9.5	9.4	9.4	9.4	4.6	9.4	9.4	9.5	9.5	9.1	9.1	9.1	9.1	9.	8.0	8.8	8.8	8.7	8.7
180	176	173.5	172	171	171	171	169	168	164.5	164.5	163.5	163.5	163.5	163.5	163.5	163.5	160	160	158.5	158.5	158.5	157.5	157.5	154	153	153	151.5	151
17		61	50	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUE=Lung;

MEDLINE=20268201; PubMed=10806482;

Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,
Betsholtz C., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;
"PDGF-C is a new protease-activated ligand for the PDGF alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
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                                                                                                                                                                                                                                                                                                                                              receptor.";

Nat. Cell Biol. 2:302-309 (2000).

-1 - SIMILARIY: CONTAINS 1 CUB DOMAIN.

EMBL; AF244813; AAF80597.1; -..

Genew; HGNC: 8801; PDGFC.

InterPro; IPRO00072; PD_growth_factor.

Ffam; PF00431; PDGF; 1.

Ffam; PF00431; PDGF; 1.

SMART; SM00441; PDGF; 1.

SMART; SM00141; PDGF; 1.

ROSITE; PS01180; CUB; 1.

ROSITE; PS01180; CUB; 1.

RPROSITE; PS0178; PDGF; 2; 1.

SRQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;
                                                         01-0CT-2000 (TIEMBLrel. 15, Created)
01-0CT-2000 (TIEMBLrel. 15, Last sequence update)
01-0MR-2003 (TIEMBLrel. 23, Last annotation update)
Platel-derived growth factor C.
Homo sapiens (Human).
                                345 AA.
                                PRT;
                                PRELIMINARY;
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01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
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SEQUENCE
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MEDLINE=21347863; PubMed=11297552;
A dilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
A dilbertson D.G., Duff M.E., Mest J.W., Kelly J.D., Sheppard P.O.,
A Hofstrand P.D., Gao Z., Sheemaker K., Bukowski T.R., Moore M.,
A Hofstrand P.D., Gao Z., Sheemaker K., Bukowski T.R., Moore M.,
Reldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
That detected drowth Factor C (PDGF-C), a Novel Growth Factor That platelet-derived Growth Factor (PDGF-C), a Novel Growth Factor T. Binds to PDGF alpha and beta Receptor.";
J. Biol. Chem. 276:27406-27414(2001).
J. Biol. Chem. 276:27406-27414(2001).
J. SIMILARITY: CONTAINS I CUB DOMAIN.
BENEL, ARC03134; AAKS1657.1;
BENEL, ARC00072; PDG domain.

RELP. ARC00072; PDG domain.

RELP. ARCONOS; PDG Growth factor.

Remai PP00141; CUB; 1.

REAM, PP00141; PDGF; 1.

REMART; SM00141; PDGF; 1.
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                                                                                         TPDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE 121
                             KEOFSSNKEQNGVODDQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL 88
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MEDLINE=20317014; PubMed=10858496;
Hamada T., Ui-Tei K., Miyata Y.;
Hamada T., Ui-Gi K., Miyata Y.;
A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
                                                                                                                                                                                     122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW
                                                                                                                                                                                                                                                                                  QLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDT
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  KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVMRLVAVEENVWIQL
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Secretary growth factor-like protein FALLOTEIN (SPINAL CORD-derived
growth factor) (Platelet-derived growth factor C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rsai Y.J., Lee R.K.K., Lin S.P.;
"Fallotein, a novel growth factor like gene identified in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEHHEECDCVCRGSTGG 318
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=Cecum, Cerebellum, and Head;
MEDLINE=22364683; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I all Team;
the RIKEN Genome Exploration Research Group Phase I all Team;
TANALYSIS of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
-!- SIMILARITY: CONTAINS I CUB DOMAIN.
EMBL, AR177608; AR722516.1; --
EMBL, AR266467; ARX58566.1; --
EMBL, AR263734; BAC28455.1; --
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Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
Gilbertson D., West J., O'Hara P.J.;
"Platelet-derived growth factor C (PDGF-C), a novel growth factor that binds to PDGF alpha receptor.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                      29 KFQFSSNKEQNGVQDPQHERIIIVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL
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0
                                                                                                                         Length 345;
                                                                                                                                                                                    Indels
PS01180; CUB; 1.
PS50278; PDGF 2; 1.
345 AA; 39029 MW; CDE9E5IF40633E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Fallotein (Platelet-derived growth factor C).
                                                                                                                         99.7%; Score 1728; DB 4; L
100.0%; Pred. No. 1.4e-161;
iive 0; Mismatches 0;
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89 TFDERFGLEDPEDDLCKYDFVEVEEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDE 148
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                                                                                                                                                                242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRPKTGVKGLHKSLTDVA 328
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            YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                              149 YFPSEPGFCIHYSIIMPQVTETTSPSVLPPSSLSLDLINNAVTAFSTLEELIRYLEPDRW
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STRAINS MICHAEL TISSUE=Kidney;

STRAINS MICHAEL TISSUE=Kidney;

MEDLINE=21092670; PubMed=11162582;

MEDLINE=21092670; PubMed=11162582;

Therefore Toning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/PDGF-C/fallotein.";

SCDGF/PDGF-C/fallotein.";

EMBL, AB03830; BAB19969.1;

SIMILARITY: CONTAINS I CUB DOMAIN.

REMBL, AB033830; BAB19969.1;

InterPro; IPR000892; PD_growth_factor.

R Pfam; PF00431; CUB; 1.

SMART; SM0042; CUB; 1.

R PROSITE; PS00141; PDGF; 1.

R PROSITE; PS00140; CUB; 1.

R PROSITE; PS00180; CUB; 1.

R PROSITE; PS00180; CUB; 1.

R PROSITE; PS00180; CUB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                             Q9EQX6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal cord-derived growth factor.
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Matches 272; Conserval
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                        Length 345;
EMBL; AK042767; BAC31358.1; -.
EMBL; AK052947; BAC35216.1; -.
NOD; MGT-1856831; PAGGE.
INTERPO: IPRO00059; CUB domain.
InterPro: IPR000072; PD_Growth_factor.
Pfam; PF00431; CUB; 1.
Pfam; PF00031; PDGF; 1.
SMART; SM00042; CUB; 1.
SWART; SM00141; PDGF; 1.
PFOSITE; PS0180; CUB; 1.
PROSITE; PS0180; CUB; 1.
PROSITE; PS0781; PDGF; 1.
PROSITE; PS0781; PDGF; 2; 1.
SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86.8%; Pred. No. 9./e-110,
tive 27; Mismatches 15; Indels
                                                                                                                                                                                                                                                      / Match 89.9%; Score 1559; DB 11; Length Local Similarity 87.1%; Pred. No. 6.1e-145; les 276; Conservative 26; Mismatches 15; Indels
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; EC037696; AAH37696.1; -.
SEQUENCE 345 AA; 38741 WW; 9A58A05C6C0E9614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Platelet-derived growth factor, C polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEHHEECDCVCRGSTGG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.84
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=CZECH II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 1
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Matches
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Query Match
Best Local Similarity
Matches 269; Conserva
                                                                                    NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 YFPSEPGFCIHYNIVMPOFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 IFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVA 301
269 IFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRPKIGVKGLHKSLTDVA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 KLQLSSDKEQNGVQDPRHERVVIISGNGSIHSPKFPHTYPRNMYLVWRLVAVDENVRTQL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 QLDLEDLYRPIWQLLGKAFVFGRKSRVVDLNLLTBEVRLYSCTPRNFSVSIREELKRTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTVPRNTVLVWRLVAVEENVWIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE
                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-SWiss-Webster/NIH;
STRAIN-SWiss-Webster/NIH;
MEDLINES-20417914; PubMed=10960785;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
Inhe mouse Pdgfc gene: dynamic expression in embryonic tissues during
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                        88.2%; Score 1530; DB 11; Length 345; 85.8%; Pred. No. 4.4e-142; tive 26; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
platelet-derived growth factor C.
                                                                                           345 AA
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                                  329 LEHHEECDCVCRGNTEG 345
                      302 LEHHEECDCVCRGSTGG 318
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.2%
Best Local Similarity 85.8%
Matches 272; Conservative
                                                                                            PRELIMINARY;
                                                                                                                                                                Mus musculus (Mouse)
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                                                                                             Q9JHV8
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Q91946
ID Q9194
AC Q9194
                                                                          RESULT 6
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345 AA

PRT;

PRELIMINARY;

Q91946 Q91946;

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REGUENCE FROM N.A.

RE SEQUENCE FROM N.A.

RY HAMBEL LEGIOTH; TISSUE=Spinal cord;

RX HAND-INE=2017014; PubMed=1058496;

RA HAMBE TO 17014; PubMed=10685496;

RT "A novel gene derived from developing spinal cords, SCDGF, is a unique RT "A novel gene derived from developing spinal cords, SCDGF, is a unique RT member of the PDGF VEGF family.";

RES Lett. 475:97-102 (2000).

CC -1. SIMILARITY: CONTAINS I CUB DOMAIN.

DR EMBL, AB033829; BAB03265.1; -.

DR INLEFPO; IPRO00092; PD Growth factor.

DR Pfam; PF00431; CUB; 1.

DR Pfam; PF0041; PDGF; 1.

DR SWART; SW00042; CUB; 1.

DR SWART; SW00141; PDGF; 1.

DR SWART; SW00141; PDGF; 1.

DR ROSITE; PS01180; CUB; 1.

DR PROSITE; PS0278; PDGF; 1.

DR PROSITE; PS0278; PDGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 IFWPLCLLIVKRCGGNCACCHQNCNECQCIPTKVTKKYHEVLQLKPRSGVRGLHKSLTDVP 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 QLDLEDLYRPTWQLLGKAYIHGRKSRVVDLNLLKBEVRLYSCTFRNFSVSLREELKRTDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 TFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERW
                                                                                                                    Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.9%; Score 1524; DB 13; Length 345; illarity 84.9%; Pred. No. 1.7e-141; Conservative 28; Mismatches 20; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-00T-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Platelet-derived growth factor C (Fragment).
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 LEHHEECDCVCRGSTGG 318
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Q9BWV5
Q9BWV5;
01-JUN-2001 (
01-JUN-2001 (
01-MAR-2003 (
    Wistow G.;
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Q9BWV5
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Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
8-PINAL CORD-derived growth factor-B (MSTP036) (IRIS-expressed growth factor long form) (Platelet-derived growth factor D).
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             ö
STRAIN-Sprague-Dawley; TISSUE-Skin;
Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
"Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                           12, Indels
                                                                    Healing.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                     258 258 29255 MW; 88625B989FCC3F8B CRC64;
                                                                                                                                                                                                                                                                                                                                                               72.7%; Score 1260; DB 11;
85.6%; Pred. No. 1.1e-115;
ative 25; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   370 AA
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                                                                                                        -i. SIMILARITY: CONTAINS I CUB DOMAIN.
ENEL; AF508348; AMM47265.1;
INTERPRO; IPRO000859; CUB_domain.
INTERPRO; IPRO00072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
SMAXT; SM00042; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS0278; PDGF_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor long form) (Platele:
HSCDGF-B OR IEGF OR PDGFD.
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.63
Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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NON TER
SEQUENCE
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LEDPEDDICKYDFVEVEREPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE 126
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                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=21231380; PubMed=11331882;
LaRochelle W.J., Jeffers M., McDnald W.F., Chillakuru R.A.,
Giese N.J., Jokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
Burges C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D. A Novel Procease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001)
-- SIMILARITY: CONTAINS I CUB DOMAIN.

EMBL, AB033832; SAB18903.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                           PubMed=11331881;
Bergsten E., Untela M., Li X., Pietras K., Ostman A., Heldin C.H.,
Alitalo K., Eriksson U.;
"PDGF-D is a specific, protease-activated ligand for the PDGF beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
42.7%; Score 741; DB 4; Length 379
Best Local Similarity 46.6%; Pred. No. 2.2e-64;
Matches 153; Conservative 52; Mismatches 93; Indels
"Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01180; CUB; 1.
PROSITE; PS50778; PDGF 2; 1.
PROSITE; PS00430; TONB DEPENDENT REC 1; 1.
SEQUENCE 370 AA, 42848 MM; D387F485E7BB7674 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AF113216; AAG3227.1;
EMBL, AF13216; AAG3227.1;
EMBL, AF33584; AAK56136.1;
EMBL; AF33584; AAK36136.1;
EMEL; AF33584; AAK36840.1;
InterPro; IPR000859; CUB domain.
InterPro; IPR00052; PD_Growth_factor.
InterPro; IPR000531; TonB_boxC.
FRAM, PF00431; CUB; 1.
SMART; SM0042; CUB; 1.
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                                                                                                                                                                                                                          receptor.";
Nat. Cell Biol. 3:512-516(2001).
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                                                                                    SEQUENCE FROM N.A.
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127
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 KLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAK 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                 136 VMPQFTEAV-----SPSVLPPSALPLDLLNNAITAFSTLEDLIRYL
                                                                                                                                                                                                                                                                                                                                              18 QHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBL_TaxID=10116;
ris-expressed growth factor short form (Spinal cord-derived growth
                                     Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                  42.6%; Score 739.5; DB 4; Length 364; 47.0%; Pred. No. 3.1e-64; ive 51; Mismatches 89; Indels 29.
                                                                                                                                                                A Straubberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AVO2518; AARX 0082.1; -.
R EMBL; BC030645; AAH30645.1; -.
R InterPro; IPR000055; CUB domain.
R InterPro; IPR000051; PD_GTOWTh factor.
R InterPro; IPR000051; TonB_boxC.
R Pfam; PF00411; CUB; 1.
R PROSITE; PS00189; CUB; 1.
R PROSITE; PS00180; CUB; 1.
R PROSITE; PS00180; CUB; 1.
R PROSITE; PS00130; TONB_DEPENDENT REC 1; 1.
                                                                                                             "Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal-cord derived growth factor-B.
RSCDGF-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 AA
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TMALVDIQLDHHERCDCIC 358
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                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 47.0%
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                  SEQUENCE FROM N.A.
TISSUE=Iris;
                                                            NCBI_TaxID=9606;
                                                                                                                                                           rissum=Testis;
                                                                                                       Wistow G.;
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              [actor-B)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
Platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN full-tength enriched library, clone:1110003109
product:platelet-derived growth factor D).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42 ESNHLTDLYRRDENIRVTGTGHVQSPRFPNSYPRNLLLTWRLHS-QEKTRIQLAFDHQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 LEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFG
MEDLINE=21092670; PubMed=11162582;

A Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

Hamada T., Ui-Tei K., Imaki J., Miyata Y.;

T "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF-Pode-C/falloten.";

Biochem. Biophys. Res. Commun. 280:733-737(2001).

- I-SIMILARITY: CONTAINS I CUB DOMAIN.

REMBL; AB052170; BAB18920.1; -

InterPro; IPR000042; PD_growth_factor.

REMBL; AB00044; CUB; 1.

SMART; SM00141; PDGF; 1.

REMBL; SM00141; PDGF; 1.

REMBL; SS011180; CUB; 1.

REMSITE; PS011180; CUB; 1.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 42.4%; Score 736; DB 11; al Similarity 45.6%; Pred. No. 6.9e-64; 149; Conservative 57; Mismatches 93.
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q92517 PRELIMINARY;
Q92517; Q9D1L8;
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Gaps

28;

94; Indels

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Matches 149; Conservative
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                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramcto K., Hiracka T., Hori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kaudi J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomira K., Numazaki R., Ohno M., Okazaki Y., Okido T., Cowa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M., Muramateu M., Hayashizaki Y., Subili GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=20530913; PubMed=11076861;
Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Suwi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Oazawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikki integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                         RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE-Body;
MEDLINE=99279253; PubMed=10349636;
Carninoi P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1919035; Pdgfd.
InterPro; IPR000859; CUB domain.
InterPro; IPR00072; PD growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-ESODY;
STRAIN-CSTRAIL/6J; TISSUE-BODY;
MEDLINE-22354683; PubMed=12466851;
The FANTOM COMBOTTIUM,
                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 409:685-690(2001).
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Length 370;

Score 736; DB 11; Pred. No. 6.9e-64;

42.4%; 45.6%;

Best Local Similarity

Query Match

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9
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                                                                                                                                                                                                                                                                                                             169 LEDLIRYLEPERMOLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNF
                                                                                                                                                                                                                                                                                                                                                                          SVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP--
                                    EQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFG
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 25.0%; Score 434; DB 11; Length 2 Best Local Similarity 41.7%; Pred. No. 2.3e-34; Matches 93; Conservative 42; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2002 (TrEMBLrel. 22, Last Sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to platelet-derived growth factor, D polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDL 211
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EMBL; BC030896; AAH30896.1; -.
MGD; MGI:1919035; Pdgfd.
InterPro; IPR000859; CUB_domain.
Pfem; PF00431; CUB.
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Mismatches
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last ann
  56;
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PROSITE; PS01180; CUB; 1.
SEQUENCE 261 AA; 30228 MW;
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Brachydanio rerio (Zebrafish) (Danio rerio).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATE LEG P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;

RA Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;

RT "Neuropilin-1 is required for normal vascular development and is a mediator of VEGF-dependent angiogenesis in zebrafish.";

RT mediator of VEGF-dependent angiogenesis in zebrafish.";

RE MEDIATITY: BELONGS TO THE NEUROPILIN FAMILY.

CC -! SIMILARITY: CONTAINS 1 MEMBRANE PROTEIN (BY SIMILARITY).

CC -! SIMILARITY: CONTAINS 1 WAM DOWAIN.

CC -! SIMILARITY: CONTAINS 1 FS/8 TYPE C DOMAIN.

DR RILLS AALAO662.1;

CN EMBL; AVO64213; AALAO662.1;

CN EMBL; AVO64313; AALAO662.1;

CN EMBL; ARO00998; WAM Gomain.

DR Pfam; PF000629; WAM Gomain.

R Pfam; PF000629; WAM Gomain.

R Pfam; PF000629; WAM: 1.

DR SMART; SM00131; PASBC; 2.

DR SMART; SM00131; MAM: 1.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01180; CUB; 2.

DR PROSITE; PS01285; FASBC 1; 1.

DR PROSITE; PS01040; MAM 1; 1.

DR PROSITE; PS00040; MAM 1; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danio.

NCBI_TaxID=7955;
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                                                                                                                                                 01-TUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Matches 60; Conserv
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86 EVRDGVDENGQLVGKYCGK-IAPSPVVSSGNQLFIKFVSD-YETHGAGFSIRYEIFKTGP 143
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes;
Cyprinidae, Danio.
NCBI_TaxIb=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 923;
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30.9%; Pred. No. 4.4e-09;
iive 26; Mismatches 87; Indels
                                                                                                                                                             SEQUENCE FROM N.A.
Shoji W., Tawarayama H.;
Shoji W., Tawarayama H.;
"The cloning and expression of neuropilin-1.";
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO84775; BACS3557.1;
SEQUENCE 923 AA; 102541 MW; 0EGCE33ED28A21F7 CRC64;
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Best Local Similarity 30.99
Matches 60; Conservative
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7

Search completed: November 25, 2003, 21:04:34 Job time: 29.0774 secs

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November 25, 2003, 22:28:25; Search time 3642.09 Seconds (without alignments) 16556.656 Million cell updates/sec
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1 cacctggagacacagaagag......aatcacaaagcactgcaccg 1474
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result 10 11 11 11 11 11 11 11 11 11 11 11 11	2 - 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	A Marter 10 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Length 2692 3512 3512 3571 3571 3571 1038 1116 1116 2825 2825 2849 2849	0 1 10 1 10 1 10 1 10 1 10 1 10 1 10 1	AK11608 AR266467 AR26281 AR262281 AR262285 AR264520 AX18787 AX18787 AX18787 AX18787 AX10624 AR210624 AR210624 AX391260 AX391260 AX391260 AX391260	Description AF117608 Mus muscu AF26467 Mus muscu AR282985 Sequence AX044520 Sequence AX18787 Sequence BC037696 Mus muscu AF286725 Mus muscu AF286725 Sequence BC037696 Sequence AX047550 Sequence AX331202 Sequence AX391260 Sequence AX391260 Sequence AX391260 Sequence AX464152 Sequence
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RESULT 1 AF117608 LOCUS DEFINITION ACCESSION VERYORDS SOURCE SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	N. L. W. M. C. J.	AF117608 Mus musculus AF117608.1 G AF117608.1 G Mus musculus Mus musculus Mus musculus I (bases I t Tsai, Y. J., L	musculus fallotei 7608. GI:665286 77608. GI:665286 musculus (house m musculus Eutheria; E 17J., Lee,R.K.	fallotein I:6652867 (house mo tazoa; Ch heria; Ro o 2692) oe, R. KK	2692 bp mRNA .n mRNA, complete cds7 .nouse) .hordata; Craniata; Ver (odentia; Sciurognathi; .K., Chen, YH., Lin, S.	linear ROD 02-JAN-2000 tebrata, Buteleostomi; Muridae; Murinae; Mus.

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          2 (bases 1 to 2692)
Tsai,Y.-J., Lee,R.K.-K., Chen,Y.-H., Lin,S.-P. and Cheng,W.T.-K.
Direct Submission
Submitted (03-JAN-1999) Medical Research, Mackay Memorial Hospit
45 Min Sheng Road, Tamshui, Taipei 25115, Taiwan
Location/Qualifiers
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. S. (2007). Hart, C., Piddington, C., Sheppard, P., Shoemaker, K., Gilbertson, D., West, J. and O'Hara, P.J.

Li Unpublished

E. (bases 1 to 3512)

E. Sheppard, P., Shoemaker, K., Gilbertson, D., West, J. and O'Hara, P.J.

Direct Submission

L. Submitted (10-MAY-2000) Biomolecular Informatics, ZymoGenetics, Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
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1 (bases 1 to 3571)
Gao, Z., Hart, C.B., Piddington, C.S., Sheppard, P.O., Shoemaker, K.E., Gibertson, D.G. and West, J.W.
Gilbertson, D.G. and West, J.W.
Growth factor homolog zvegf3
Patent: US 6528050-A 42 04-MAR-2003;
Location/Qualifiers
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Gilbert,T., Hart,C.E., Sheppard,P.O. and Gilbertson,D.G.
Growth factor homolog zvegf4
Patent: WO 0066736-A 34 09-NOV-2000;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Method of treating fibrosis
Patent: WO 0128586-A 3 26-AER-2001;
ZymoGenetics, Inc. (US)
ZymoGenetics, Inc. (US)
Location/Qualifiers
1..3571
//mol type="genomic DNA"
//mol type="genomic DNA"
//db xref="taxon:10090"
//db xref="taxon:10090"
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Mus musculus
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Best Local Similarity 99.4%;
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                                                         1035 CCCCAGTCAGCCAAATGCTCCTCCTGGCCTCCTCCTGCTGACATCTGCCCTGGCCGCGC
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Mus musculus (house mouse)

Mus musculus (house mouse)

Bukaryoza; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus musculus

Bukaryoza; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

E (bases 1 to 2731)

Straubberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collina,F.B., Wagner,L., Shemmen,C.M., Schuler,G.D.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant, T.L.,

Stapleton,M., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalon,D.K., Muzuy,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Racky, K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Pahey,J., Helton,B., Ketteman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marre,M.A.

Generation and initial analysis of more than 15,000 full-length
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Mus musculus platelet-derived growth factor, C polypeptide, mRNA
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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      Contact: nisc mgc@nhgri.nih.gov
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Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.H. and Green,B.D.
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                                                                                                                                                                                                                                                                                                                  clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 80 Row: f Column: 13
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10242384.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="Mammary tumor metastatized to lung.
MMTV-LITE/Wht1 model. Expression driven by an MMTV-LTR
enhancer."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: 1110064L01Rik"
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/db_xref="MGI:1859631"
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="NCI CGAP_Lu30"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
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| gene="POGFC; similar to PDGF/VEGF"
| foote="POGFC; similar to PDGF/VEGF"
| codon_start=1 |
| codon_start=1 |
| product="platelet-derived growth factor C" |
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Mus musculus platelet-derived growth factor C (Pdgfc) mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ding, H., Wu, X., Tam, P.P.L. and Nagy, A. Ding, H., Wu, X., Tam, P.P.L. and Nagy, A. Direct Submission Submission Shmitted (12-JUL-2000) Samuel Lunenfeld Research Institute, Mount Shai Hospital, 600 University Avenue, Toronto, Ontario MSG 1XS, Canada
9
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I Dasea I to 1038.
Ding.H., Wu,X., Kim,I., Tam,P.P., Koh,G.Y. and Nagy,A.
The mouse Pdgfc gene: dynamic expression in embryonic tissues
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larity 99.4%; Pred. No. 2.8e-288;
Conservative 0; Mismatches 6; Indels 0;
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    1038
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Swiss-Webster/NIH"

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                                                             ACCAANAGGAGTCAATCACAAAGCACTGC 1470
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Mech. Dev. 96 (2), 209-213 (2000)
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AB033830 GI:11994799 Spinal cord-derived growth factor; SCDGF.
Spinal cord-derived growth factor; SCDGF.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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181 ccgaagiriccicaracaracccaagaaararggrecregregregagarracregas
                                                                                                                                 GATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGCTGGAAGATCCCAGAA
                                                                      241 GATGAAATGTGCGGACCCAGCTGACATTTGATGAGAGTTTGGGCTGGAAGACCCCAGAA
                                                                                                              GACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCCAGTGATGGAAGTGTTTTA
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GGAAACGCAGGGAAACTGCAGGCTTCGTAGCAGCACGTGAGCACTGGCATTCTGT 1275
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Hamada,T., Ui-Tet,K. and Miyata,Y.
Direct Submission
Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,
                                                                                                                                                                                                                                                                                                                                                                                                                                               CATAAGTCACTCACTGATGTGGCTCTGGAACACCACGAGGAATGTGACTGTGTGTAGA
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                AGTATTATCATGCCACAAGTCACAGAAACCACGAGTCCTTCGGTGTTGCCCCCTTCATCT
                                                                         TTGTCATTGGACCTGCTCAACAATGCTGTGACTTCCAGTACCTTGGAAGAGCTGATT
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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A novel gene derived from developing E unique member of the PDGF/VEGF family FEBS Lett. 475 (2), 97-102 (2000)
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spinal cord-derived growth
Homo sapiens (human)
Homo sapiens
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/product= spinal cord-derived growth factor"
/protein_id="Bab19969.1"
/db_xref="di:11994800"
/translation="WLILGILLITSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDP
RHERYVTISGNGSLHSPRFPHTYPRNTVLVWRLVAVDENVRICHTBERGLEDPEDD
RCHORYVETSERSDGSVLGRRGGSGTVPGRCTSRGNHTRIRFVBDEYFPSEPGFCHYV
SIIMPQVTETTSPSVLPPSALSLDLINNAVTRASTVEELIRFLEPDRWQIDLDSLYKP
TWPLLGRAFIYGKKSRAVNLNLKEEVTASCTPRNFSVSIREELKRTDTIFWPGCLL
VKRCGGNCACCLHNCNBCQCVPRKYTKKYHEVLQLRPRIGVKGLHKSLTDVALEHHEE
CDCVCRGNTEG"
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       1 (sites)
Hamada,T., Ui-Tei,K., Imaki,J. and Miyata,Y.
Molecular cloning of SCDGF-B, a novel growth factor homologous SCDGF-DGF-C/fallotein
Biochem. Biophys. Res. Commun. 280 (3), 733-737 (2001)
                                                                                                                              Coases 1 to 1116)

Hamada,T., Ui-Tei,K. and Miyata,Y.

Hamada,T., Ui-Tei,K. and Miyata,Y.

Direct Submissor.

Submitted (25-OCT-1999) Tsuyoshi Hamada, Nippon Medical School,

Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo

113-8602, Japan (E-mail:t-hamada@nms.ac.jp,

Tel:81-3-3822-2131(ex.5277), Fax:81-3-8814-1684)
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1020.8; DB 10; Length 1116;
Pred. No. 4.6e-286;
0; Mismatches 52; Indels 1; C
                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wistar"
                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10116"
/tissue_type="Kidney"
/dev_stage="Adult"
1. 1116
 Eutheria; Rodentia;
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1. .1038
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Best Local Similarity 95.3%;
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Patent: US 6391311-A 1 21-MAY-2002;
Location/Qualifiers
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                  Department of Pharmacology; 1-1-5, Sendagi, Bunk; 113-8602, Japan (E-mail:t-hamada@nms.ac.jp, Tel:81-3-3822-2131(ex.5277), Fax:81-3-5814-1684) Location/Qualifiers
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Pred. No. 6.4e-255;
0; Mismatches 203;
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Ferrara,N. and Kuo,S.S.
Nucleic acids encoding vascular endothelial cell growth factor-E (VEGF-E)
                                         TGTGACTGTGTGTAGAGGAAACGCAGGAGGGTAACTGCAGCCTTCGTAGCAGCAC 1254
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                              CCCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCCAGTGCAGCCTTCCC
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Score 914.2; DB 6; Length 2849;
Pred. No. 7e-255;
0; Mismatches 203; Indels 4;
  Query Match 62.0%;
Best Local Similarity 83.5%;
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Compositions and methods for the treatment of immune related
                             TCTAAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCCTTCTGAACCA 720
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genentech, Inc. (US)
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Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara, N., Williams, P.M., Baker, K.P., Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L., Kuo, S.S., Mark, M.R., Marsters, S.A., Pitti, R.M., Wood, W.I., Gerber, H., Gerritsen, M.E., Paoni, N.F. and Watanabe, C.K.
Promotion or inhibition of angiogenesis and cardiovascularization Patent: WO 0073445-A 3 07-DEC-2000;
Genentech Inc. (US)
Location/Qualifiers
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Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.
Wood,W.L. and Itansmembrane polypeptides and nucleic acids encoding
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Pred. No. 7e-255;
0; Mismatches 203;
                                                                                                     Patent: WO 0140466-A 285 07-JUN-2001;
Genentech Inc. (US)
Location/Qualifiers
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                     Run on:
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SUMMARIES

Description	cDNA encoding muri	Mouse zvegf3 DNA,	Murine vascular en	Mouse Zvegf3 DNA.	Mouse cDNA encodin	Mouse zvegf3 codin	DNA encoding mouse	Human VEGF-X DNA i
QI	AAA12525	AAC81583	AAA51527	AAD04650	ABS68648	AAI 72444	ABX93182	AAA71955
80	21	21	21	22	24	24	25	21
% Query re Match Length DB ID	1474	3571	3571	3571	3571	3571	3571	1473
% Query Match	99.9	98.0	98.0	98.0	98.0	98.0	98.0	62.0
Score	1473	1444.8	1444.8	1444.8	1444.8	1444.8	1444.8	914.2
Result No.	1	74	m	4	_C	9	7	60

102			ğ	Human LP8, a PDGF-	TANGO			PRO200	PR0200		CDNA 8	PR0200	Human PRO200 codin	Human anglogenesis	cDNA encoding huma	Human cDNA encodin	DNA encoding novel	cDNA encoding huma	Human platelet-der	DNA encoding numan	DNA encoding for n	cDNA encoding huma	norphog	VEGF-X	zvegt3	growth	Zvegt	cDNA en		m	ancer		Human VEGF/PUGF-11	7.	morphogenic	cDNA encoding plat
AB081461	AAA71990	AAZ23691	ABS57294	AAD06812	AAA47452	AAZ34296	AAC78582	AAA88515	AAC58579	AAA77621	AAS21386	AAC90564	AAC88962	AAC97404	ACA03745	ACA04166	ABX89283	ABX92668	AAC64426	AAX86352	AAS12884	AAA52458	AAZ48599	AAA71952	AAC81582	AAA51498	AAD04649	ABS68612	AAI72443	ABX93146	AAF18314	AAA71951	AAF82259	ABN88974	AAZ48600	AAA12523
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ALIGNMENTS

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Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VBGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling; ss.
                                                                                     CDNA encoding murine platelet-derived growth factor C (PDGF-C)
                                                                                                                                                                                                                                         /*tag= a
/product= "platelet-derived growth factor C"
                                                                                                                                                                                                               Location/Qualifiers
196..1233
                    AAA12525 standard; cDNA; 1474 BP
                                                                                                                                                                                                                                                                                                                                                  98US-0102461.
98US-0108109.
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                                                                    25-JUL-2000 (first entry)
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12-NOV-1998;
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CC and/or growth or motility of cells expressing a PDGF-C receptor.

CC proliferation, preferably in combination with one other growth factor or haramequaticals comprising PDGF-C polypeptides can also be used for stimulating commetive tissue or wound healing. The CC prolipeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C. PDGF-C can also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation.

CC pDGF-C antagonists can be used to inhibit tumnours engine through a tumour control or control or structum and the polyperic polyperic can be used to inhibit tissue control of conditions, and erythroleusemia, can be identified by testing for expression of remodelling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to inhibit tissue

CC calls, Antagonists can also be used to inhibit tissue

CC calls, Antagonists can also be used to inhibit tissue
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                                                                                                                                                                                                                                                                                                              Uutela M,
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                                                                                                                                                                                                                                                                                                Lee X, Ponten A,
Betsholz C;
                                                                                                                                                                                                     LUDWIG INST CANCER RES.
UNIV HELSINKI LICENSING LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 5; 135pp; English
                             98US-0110749.
98US-0113002.
99US-0135426.
99US-0144022.
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Heldin C,
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P-PSDB; AAY84559.
                                03-DEC-1998;
18-DEC-1998;
21-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                          Oestman A,
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Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; murine; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver amage; neuroregenerative; Alienimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia;
                                                                                                                                                                                                                                                              Gilbertson DG
                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 127-130; 143pp; English
                                                                                                                                                                                                                                                              Sheppard PO,
                                                                Mouse zvegf3 DNA, SEQ ID NO:34
                                                                                                                          immunomodulation; hepatic; ds
               AAC81583 standard; DNA; 3571
                                                                                                                                                                                                            03-MAY-1999; 99US-0304216.
10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
                                                                                                                                                                                             03-MAY-2000; 2000WO-US40047
                                                (first entry
                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                  e.g. for treating live
Alzheimer's disease –
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                                                                                                                                                                                                                                                                              WPI; 2000-687541/67.
P-PSDB; AAB48658.
                                                                                                                                                           WO200066736-A1
                                                09-MAR-2001
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                                                                                                                                                                                                                                                              Gilbert T,
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                                 AAC81583;
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        AAC81583
RESULT
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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

of the PDGF (platelet-derived growth factor)/YGBF (vascular endothelial

growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

characterised by a PDGF cystine knot structure, and a CUB domain

(AAB48655) which has a beta barrel structure. Zvegf4 has PDGF-like

activity, having mitogenic activity on fibroblasts, vascular smooth

muscle cells and pericytes, and has also been shown to stimulate bone

cyprowth. The invention also relates to fusion proteins comprising human

zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4

cyprosphi to human zvegf4 or a fragment thereof; a method of a city which binds to human zvegf4 or a fragment thereof; a method of a city which binds to human zvegf4 or a fragment thereof; a method of a city at no comprising exposing bone cells to method ism of bone cells, comprising exposing bone cells to comprising exposing bone cells

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cypf4-derived polypopt used to enhance expansion and mobilisation of haematopoietic stem cells and endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents DNA encoding mouse factor homologs and the nucleic acids that encode them, useful or treating liver damage, ischemia, multiple sclerosis and

zvegf3

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                                                                                                                98.0%;
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                     1875 redrehadederigideadeadarrerecergrigicicearaarrecaargaargicaer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vascular endothelial growth factor; homologue; zvegf3; CUB domain; Cysteine knot; platelet-derived growth factor; PDGF; neuropilin; chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine vascular endothelial growth factor homologue, ZVEGF3 DNA.
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factor homologue. Polypeptides comprising an epitope-bearing portion human or murine ZVEGF3 are claimed. The growth factors comprise a growth factor domain and a CTB domain (generic sequence motifs are shown in AAY96869) and AAY96860). The growth factor domain is characterized by an arrangement of Gysteine residues and beta-strands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domains shows homology to CUB domains in neuropilins, human bone morphogenetic protein. In portine seminal plasma protein, bovine acidic seminal fluid protein and Xenopus laevis protein. Structural analysis and homology predict that close proteins. The human zvegf3 gene has been mapped to chromosome 4Q28.3 crostins. The human zvegf3 gene has been mapped to chromosome 4Q28.3 croteins. The human zvegf3 gene has been mapped to chromosome 4Q28.3 croteins. The human zvegf3 gene has been mapped to chromosome 4Q28.3 croteins. The human zvegf3 gene has been mapped to chromosome 4Q28.3 croteins are useful for stimulating the growth of fibroblasts or smooth cuseful for regulating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZvegF3 antegonists are useful for treating cancer, rheumatoid architis, dischemia, vascular intimal hyperplasia, disease, mycocardial ischemia, vascular intimal hyperplasia, disease and haemangioma for formation. ZVEGF3 can also be used to modulate neurite growth and for elementative and for treating neurodegenerative
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                                                                                                                                                               Novel rvegf3 polypeptides and nucleotides encoding them useful for stimulating growth of smooth muscle cells and fibroblasts comprising epitope bearing portion of a specific amino acid sequence
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AAD04650;

(first entry) 04-JUL-2001

Zvegf3 Mouse

extracellular matrix production; fibrosis; VEGF-R; PDGF-C; platelet-derived growth factor; PDGF; vascular endothelial growth factor; VEGF, mitogenic effect; therapy; keloid; scleroderma; fibrotic disorder; chronic active hepatitis; fulminant viral hepatitis; amyloidosis; diabetic nephropathy; alpha-l-antitrypsin deficiency; silicosis; asbestosis; renal arterioscalerosis; post necrotic cirrhosis; diabetic glomerulosclerosis; focal glomerulosclerosis; hyperosics; pulmonary hypertension; idiopathic pulmonary fibrosis; osteopetrosis; bronchiolitis obliterans organising pneumonia; transplant vasculopathy; etheracolitics. Zvegf3 antagonist; cell proliferation; stellate cell activation; fibroproliferative disorder; ds

musculus

/product= "Mouse Zvegf3 protein" Location/Qualifiers 1049..2086 /*tag= a

WO200128586-A1

26-APR-2001

23-OCT-2000; 2000WO-US29270

21-OCT-1999; 99US-0161653. 12-NOV-1999; 99US-0165255. 01-AUG-2000; 2000US-0222223.

(ZYMO) ZYMOGENETICS INC

Gilbertson DG;

2001-300278/31. P-PSDB; AAE00998

oŧ Use of zvegf3 antagonist for reducing fibroproliferative disorder kidney, liver and bone, reducing extracellular matrix production, treating fibrosis or reducing stellate cell activation in mammal

Example 2; Page 58-61; 70pp; English

The patent discloses materials and methods for reducing cell
proliferation or extracellular matrix production, treating fibrosis and
ceducing stellate cell activation in a mammal. The method comprises
administering a composition containing a Zvegf3 antagonist in combination
with a delivery vehicle. The Zvegf3 is a protein that is structurally
celated to platelet-derived growth factor (PpGP) and the vascular
endothelial growth factors (VEGP). The Zvegf3 protein is also designated
as "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the
mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
keloids, scleroderma, fibrotic disorders of liver such as chronic active
centry fulminant viral hepatitis, post necrotic cirrhosis and
alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
centry amyloidosis and renal atteriosclerosis, fibrotic disorders
of the lung such as silicosis, asbestosis, idiopathic pulmonary hypertension,
fibrotic disorders of pancreas, fibroproliferative disorders of the
changed and as transplant vasculopathy and fibroproliferative
disorders of the bone such as osteopetrosis and hyperostosis. The present sequence is mouse Zvegf3 DNA

Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;

RESULT 4
AAD04650
ID AAD0

AAD04650 standard; DNA; 3571

Length 3571; DB 22; 98.0%; Score 1444.8;

Query Match

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chromosome 3; cell proliferation; differentiation; metabolism; chromosome 3; cell proliferation; differentiation; metabolism; migration; revaecularisation; solid tumour; diabetic retinopathy; psoriasis; rheumatoid arthritis; cancer; autoimmune disease; inflammation; myocardial ischaemia; scleroderma; fibrosis; mouse; glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn; skin grafting; female reproductive tract disorder; chromic liver disease; circulatory disorder; heart fallure; neurodegenerative disease; multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
                                                                                                                                                                                                                                                            2235 TIGITITGCTICAATAGCCTICCCCTGCAGGACTICAAGTGTCTTCTAAAAGACCAGAGGC
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                                 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCACGAGGAATGTG
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useful for treating skin wounds, reproductive tract disorders, Novel polypeptide, designated zvegf3 useful for ulcers, burns, skin grafting, female reproducti Parkinson's disease, and Alzheimer's disease –

Example 4; Column 97-104; 68pp; English

The invention relates to an isolated polypeptide, designated zvegf3

(a vascular endothelial growth factor-like protein) of 111-136 amino acid

(a vascular endothelial growth factor-like protein) of 111-136 amino acid

(a vascular endothelial growth factor-like protein) of 111-136 amino acid

(comprising a first polypeptide disulphide bonded to a second

protein comprising a first polypeptide disulphide bonded to a second

polypeptide, where each of the first and second polypeptides is from

condition, metabolism or migration, the zvegf 3 encoding

condition, metabolism or migration, the zvegf 3 encoding

colymucleotides and zvegf 3 expression vectors and host cells.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Promoting growth of bone, ligament or cartilage in a mammal, involves administering to the mammal a protein which comprises growth factor domain of zvegf3 protein, a homolog of platelet-derived growth factor
                                                                                                                                                                                                                                                                                       Gene; human; mouse; zvegf3; zvegf4; platelet derived growth factor; PDGF; homolog; growth; bone; ligament; cartilage; proliferation; osteoblast; chondrocyte; bony defect; fracture; bone graft; implant; periodontal pocket; osteoclast; bone marrow stem cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3571 BP; 876 A; 935 C; 875 G; 885 T; 0 other;
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21-OCT-1999, 99US-16553P.
12-NOV-1999, 99US-165255P.
31-MAR-2000, 2000US-193732P.
07-DEC-1999, 99US-0457066.
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(GILB/) GILBERTSON D G.
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Score 1444.8; DB 24; Length 3571; Pred. No. 0;

98.0%; 99.4%;

Query Match Best Local Similarity

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1574
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                                               CCCTGCGATTCTCTGCTGCCAGAGCCAGGCGCTTCCACCGCAGCGCAGCCTTTCCC
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GIGICCIALGIAAAGITACAAAAAAGIACCATGAGGICCITCAGITGAGACCAAAAACIG 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory disorder; rheumatoid arthritis; vasculogenesis; angiogenesis; nervous system disorder; cytostatic; hepatotropic; vulnerary; tranquilliser; cerebroprotective; neuroprotective; nootropic; ophthalmological; dermatological; coagulant; cardiant; chromosome 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; growth factor homologue; zvegf3; fibroblast; smooth muscle cell; cell-surface platelet-derived growth factor alpha receptor; PDGF; full-thickness skin wound; female reproductive tract; duddenal ulcer; prolonged bleeding; periodontal disease; tissue adhesive; liver damage; revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis; chronic active hepatitis; hepatic chronic passive congestion; stroke; central haemorrhagic mecrosis; hepatic vein thrombosis; ischaemia; portal vein thrombosis; cardiac sclerosis; new vessel formation; endothelial precursor stem cell; neovascularisation; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organ transplant; tissue grafting; peripheral neuropathy; spinal cord; sensory neurite outgrowth; brain damage; head injury; paralysis; spinal injury; neurodegenerative disease; diabetic retinopathy; psoriasis; arthritis; scleroderma; keloid; liver fibrosis; psoriasis; lung fibrosis; kidney fibrosis; glomerulosclerosis; cancer; proliferative vascular disorder; ocular neovascularisation;
                                                                                                                                     2055 ACTGTGTGTGTGTAGAGGAACGCAGAAGGGTAACTGCAGCCTTCGTAGCAGCACACGTGAG
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                                                                 1995 GAGTCAAGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCCACGAGGAATGTG
                                                                                                                                                                               CACTGGCATTCTGTGTACCCCCACAAGCAACCTTCATCCCCACCAGCGTTGGCCGCAGGG
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                                   GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCACGAGGAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding mouse growth factor homologue, zvegf3.
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/product= "Zveg£3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX93182 standard; DNA; 3571
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The present invention relates to the isolation of a growth factor concoling it. The zvegf3 polypeptide is useful for stimulating the encoding it. The zvegf3 polypeptide is useful for stimulating the encoding it. The zvegf3 polypeptide is useful as a prof apha receptor agonist and cell-surface platelet-derived growth factor (PDGF) alpha receptor. The zvegf3 polypeptide is useful as a PDGF alpha receptor agonist and cell-surface platelet-derived growth factor (PDGF) alpha receptor. The zvegf3 polypeptide is useful as a PDGF alpha receptor agonist and certain full-thickness skin wounds, female certain full-thickness skin wounds, female certain in tissue adhesives for promoting the sam additive in tissue adhesives for promoting cuseful as an additive in tissue adhesives for promoting cuseful as an additive in tissue adhesives for promoting cuseful certical hepaticis, hepatic chronic passive congestion disease, chronic active hepatitis, hepatic chronic passive congestion (CPC), central haemorrhagic necrosis (CHN), hepatic vein thrombosis, cordiac sclerosis, and many types of cirrhosis. CC portal vein thrombosis, cardiac sclerosis, and many types of cirrhosis. CC conduction in areas requiring neovascularisation and mobilisation of endothelial precursor stem cells, creating and stabilising new vessel conduction in areas requiring neovascularisation, including areas of cirrhosis. CC cord and sensory neurite outgrowth, and as part of therapeutic creament for the regeneration of neurite outgrowths following strokes, cord and sensory neurite outgrowth, and as part of therapeutic creament for the regeneration of neurite outgrowths following strokes, coliseases (e.g. multiple sclerosis, Alzheimer's disease, Parkinson's disease), diabetic retinopathy, psoriasis, arthritis, scleroderma, and cirrhosis, and glomerulosclerosis. An antibody that binds reading fibrosis, and glomerulosclerosis. An antibody that binds arthritis, influenced to require the profession of the patelon of arthritis, and for treating proliferative valessab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CGGGCTGGGCCTTGGAGTCGTCGCTTCCCCAGTGCCCGCGAGTGAGCCCTCG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           necvascularisation, inflammatory disorders, rheumatoid arthritis, psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis, and diseases of the nervous system. The present sequence encodes
                                                                                                                                                                                                                                                                                                                    New isolated zvegf3 polypeptide, useful for treating cancer,
Alzheimer's disease, Parkinson's disease, chronic active hepatitis,
hepatic vein thrombosis, comprises growth factor domain and CUB domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTGCGCATTCTCTGCTGCCAGAGCCGGCCAGGCGTTCCACCGCAGCGCAGCCTTTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.0%; Score 1444.8; DB 25; Length 3571; 99.4%; Pred. No. 0;
                                                                                                                                                                                        Shoemaker KE;
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                                                                                                                                                                                           Hart CE, Piddington CS, Sheppard PO,
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0; Mismatches
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                98US-111173P.
99US-142576P.
99US-161653P.
99US-165255P.
99US-0457066.
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                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                       West JW;
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Best Local Similarity
                                                                                                                                                                                                                                                                   WPI; 2003-328485/
P-PSDB; ABG76398
                                                                                                                                                                                                                    Gilbertson DG,
                     07-DEC-1998;
06-JUL-1999;
21-OCT-1999;
                                                                                      12-NOV-1999;
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skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence encodes the human VBGF-X protein isolated from clones 4 and 7 described in the method of the invention.
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                                                                                                               Score 914.2; DB 21; Length
Pred. No. 1.1e-267;
0; Mismatches 203; Indels
                                                                                  Sequence 1473 BP; 406 A; 321 C; 361 G; 385 T; 0 other;
                                                                                                                  Query Match
Best Local Similarity 83.5%;
Matches 1050; Conservative
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1077 1137 1198 TGTGACTGTGTGTAGAGGAAACGCAGGAGGTAACTGCAGCCTTCGTAGCAGCAC 1254 CAGTGTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAA GIGGIGGAICTGAACCITCTAACAGAGGIAAGATTATACAGCTGCACACCTCGTAAC TTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACGAACCGATACTTCTGGCCAGGTTGT CICCTGGTTAAACGCTGTGGGGGAACTGTGCCTGTTGTTCTCCACAATTGCAATGAAGG TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT Vascular endothelial growth factor-X; VEGF-X; platelet-derived growth factor-C; PDGF-C; human; smooth muscle; cell proliferation; tissue repair; antiarteriosclerotic; vulnerary; vasotropic; uropathic; gene therapy; chromosome 4q31-q32; gene; ss. event" event" event" /note= "location of predicted mRNA splicing event" event" splicing splicing splicing mRNA splicing /*tag= i
note= "cryptic splice donor/acceptor site"
1165..1166 *tag= f
note= "cryptic splice donor/acceptor site" mRNA predicted mRNA mRNA Human vascular endothelial growth factor-X cDNA predicted predicted predicted /*tag= d /note= "location of p: 568.569 /*tag= | Location/Qualifiers 257..1294 //trag= a //trag= a 257..322 /*tag= b 323..1291 /*tag= c 363..364 '*tag= g 'note= "location of φ '*tag= h 'note= "location BP CDNA; 2632 (first entry) 03..704 744..745 942..943 979..980 *tag=

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CGG----GCTGGGCTTGGAGTCGTCGCTTCCCCAGTGCCCGCGCGAGTGAGCC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the CDNA sequence of human vascular endothelial growth factor-X (VEGF-X), or platelet-derived growth factor-C (PDGF-C), a novel member of the VEGF/POGF family. The cator-C (PDGF-C), a novel member of the VEGF/POGF family. The cDNA was obtained from a search of expressed sequence tag databases. Positions of mRNA splicing events were determined either from direct sequencing on an isolated BAC clone or by comparison of partial BAC database sequences. No information on splicing events is available for the region from nucleotides you to 957. Cryptic splice donor/acceptor sites were deduced from variant sequences isolated by PCR. The VEGF-X gene was localised to the long arm of human chromosome 4, region q1-q32. The VEGF-X protein, and its CUB domain, exhibit a mitogenic activity on human smooth muscle cell. Claimed methods of treating or preventing a urethral dysfunction, bladder dysfunction, pelvic floor reconstruction, sphincter dysfunction or a dysfunction associated with aberrant endogenous VEGF-X activity comprise administering a conceing it, an expression vector comprising the nucleic acid molecule or apharmaceutical composition comprising the nucleic acid molecule or apharmaceutical composition comprising the nucleic acid molecule or polypeptide. Claimed methods of treating or preventing atherosclerosis, neointimal hyperplasis caused by artery anastomosis or balloon catheter, post-angioplasty regrenosis cornary anastomosis or balloon catheter, post-angioplasty regrenosis and planed with smooth muscle cell proliferation, and condition, as susceptibility to such a condition, associated with smooth muscle cell proliferation, are also claimed.
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Pred. No. 1.6e-267;
0; Mismatches 203;
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Matches 1050; Conservative
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P-PSDB; AAB10644
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2000-442669/38.

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VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; antiologenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gosiewska A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dijkmans JJH,
                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                              "VEGF - X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        You JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-0028377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (JANC ) JANSSEN PHARM NV
  (first
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                                        CDNA
                                                                                                                                                                                                                                                                                                                                                     WO200037641-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1998;
18-MAR-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SN,
                                                                                                                                                                                                                                                                                                                                                                                                                                   21-DEC-1999;
                                      Human VEGF-X
                                                                                                                                                                                                                    sapiens
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19-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gordon RD,
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                                                                                                                                                                                                                    Ношо
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New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -Disclosure, Fig 30B; 127pp; English

This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary cytostatic, antirheumatic, antiantitic, antipsoriatic and antidiabetic activity and acts as an anglogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic ethinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcars, pressure sores, venous sores, diabetic ulcars and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence encodes a human VEGF-X protein described in the method of the invention.

Seguence 2668 BP; 780 A; 511 C; 567 G; 810 T; 0 other;

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62 CCCTGCGATTCTCTGCTGCCAGACCGGCGCGTTCCACCGCAGCGCAGCGTTTCCC 121
129 CCCTGCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCC 188
                                                                                                                                    AACTGGAGACACACAGAAGAGGGCTCTAGGAAAAGTTTTGGATGGGATTATGTGGAAACTA 128
                                                                                                          61
                                                                                                       ACCTGGAGACACAGAAGAGGGCTCTAGGAAAAATTTTGGATGGGGATTATGTGGAAACTA
                                                         Gaps
62.0%; Score 914.2; DB 21; Length 2668; 83.5%; Pred. No. 1.6e-267;
                                                         4;
                                                      Indels
                                                      0; Mismatches 203;
                                                   Matches 1050; Conservative
                            Best Local Similarity
                                                                                                                                                           69
       Query Match
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à g ò g

1137 1197 1017 1077 1268 1028 1088 1148 1208 848 548 537 608 597 668 657 728 717 788 777 837 908 897 968 957 248 237 308 297 368 357 428 417 488 477 ACTGGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCCACGAGGAA 1209 ACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAG AATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATACGGTCTTGGTA GGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCC AGTGATGGAAGTGTTTTAGGACGCTGGTGTGGTTCTGGGACTGTGCCAGGAAAGCAGACT AGTGATGGAACTATATAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAACAGATT TCTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC rcraaaggaaarcaaarraggaraagarrrgrarcrgargaararrrccrrcrgaacca GGATTCTGCATTCCACTACAGTATTATCATGCCACAAGTCACAGAAACCACGAGTCCTTCG GTGTTGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACAATGCTGTGACTGCCTTCAGT ACCTIGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC 909 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTGGAAGAAAATCCAGA GTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAAC 969 Grocrocarcrida a controla a cada contra a contra cada controla controla de controla a controla TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT 1029 TTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGT 1089 crecingerrahaccererecreseahererecererrereceaningahrer CAGTGTCCCCACGTAAAAGTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAA AATGGGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAAGAAATATGGTGCTGGTG Grischacicicitricascitrigicacidescriscitralararacidescritrast ----GCTGGGCTGAGCCTTGGAGTCGTCGCTTCCCCAGTGCCCGCGCGAGTGAGCC CTCGCCCCAGTCAGCCAAATGCTCCTCCTCGCCTCCTCCTGCTGACATCTGCCCTGGCC GGCCAAAGAACGGGGACTCGGGCTGAGTCCAACCTGAGCAGCAAGTTGCAGCTCTCCAGC GGGCTGGAAGATCCAGAAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCC GACAAGGAACAGAACGGAGTGCAAGATCCCCGGCATGAGAGAGTTGTCACTATATCTGGT TGGAGATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTT 9 1149 1138 838 1078 928 1018 249 298 369 358 429 418 549 538 609 598 699 658 729 718 789 778 868 238 489 478 178 셤 셤 g g 셤 ਨੇ ద à 셤 ò a ð 유 δ 셤 ठे 유 à 셤 Š ઢ Š 셤 셤 ద à ద à ò à ઠ ठे

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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has cranginalizer, vulnery and cardiant activity. VEGF-E can be administered the tranquillizer, vulnery and cardiant activity. VEGF-E can be administered the amount of the superior in mammals, especially by expressing encoding polynucleotides, to treat cardiavascular or endothelial disorders in mammals, especially cangeneration, and may especially be used to treat cardiac hypertrophy can be combined with a carrier in pharmaceutical compositions, which can be combined with a carrier in pharmaceutical compositions, which can be combined with a carrier in pharmaceutical compositions, which care angiogenic disorders in mammals (especially humans) e.g. cancer or serven for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (e.g. useful therapeutically as antagonists, as above. The antibodies are also useful therapeutically as antagonists, as above and the antibodies are also cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vaccular disease, or neovascularization associated with tumor formation) by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polymorleotides encoding UEGF-E can be used to diagnose cardiovascular and endothelial disease or in mammals, by detecting abnormally high or low VEGF-E gene expression in the succession in th
                                                                                                                                                                                                                                                                                                                                                VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a
                           TGTGACTGTGTGTAGAGGAAACGCAGGAGGGTAACTGCAGCCTTCGTAGCAGCAC 1254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New growth factor polypeptide useful for treating cardiovascular endothelial disorders, e.g. cardiac hypertrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
259..1296
/*tag= a
/product= "VEGF-E"
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                                                                                                                                                                standard; DNA; 2825
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98US-0184216
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P-PSDB; AAY33679.
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                                                                                                                                                                                                                                                                                                           Human VEGF-E DNA.
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02-NOV-1998;
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                    sequences or for gene mapping. This sequence encodes the human VEGF-E protein described in the method of the invention.
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sample. They may also be used to produce probes useful to detect sequences or for gene mapping. This semisance
                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                               Length 2825;
                                                                                                                                      Seguence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;
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es 203;
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83.5%; Pred. No. 1.7e-
ive 0; Mismatches
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Matches 1050; Conservative
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in wound repair, as well as in the generation and regeneration of tissue. The sequences of the invention are useful for diagnosing or treating cardiovascular, endothelial or angiogenic disorders such as cancer, diabetes mellitus, cardiac hypertrophy and atherosclerosis. The polymucleotide encoding VEGP-E is useful in the gene therapy of such disorders. The present sequence encodes human VEGF-E.
                                                                                                                                                                                   Score 914.2; DB 25; Length
Pred. No. 1.7e-267;
0; Mismatches 203; Indels
                                                                                                                                                Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;
                                                                                                                                                                                         Query Match 62.0%;
Best Local Similarity 83.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; vascular endothelial cell growth factor-E; VEGF-E; PR0:200; VEGF; bone morphogenetic protein 1; wound repair; tissue regeneration; cardiovascular disorder; endothelial disorder; angiogenic disorder; cancer; diabetes mellitus; cardiac hypertrophy; atherosclerosis; cardiant; cytostatic; antidiabetic; antiarteriosclerosis; gene therapy; gene; ds.
                                                                                                                                       CAGTGTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAA
                                TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT
                                                                                                              CTCCTGGTCAAGCGCTGTGGAGAAATTGTGCCTGTTGTCTCCCATAATTGCAATGA
                                                                  rrcrcagraccaraagggaagaacraagggaaccgaraccarrrrcrggccaggragr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human vascular endothelial cell growth factor-E (VEGF-E)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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  treating bone fractures
fragment is useful for promoting bone growth, treating bone fractures prophylactically increasing or maintaining bone density in a subject having a substantially normal bone density, so as to stimulate osteoblast proliferation, treating osteoporosis, muscle or bone loss due to malignancy, endocrine disorder, arthritis, sarcopenia and periodontal disease, preventing cartilage differentiation, and
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Pred. No. 1.7e-267;
0; Mismatches 203;
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                                                                                                                      Sequence 2827 BP; 864 A; 522
                                                                                                                                               Query Match 62.0%;
Best Local Similarity 83.5%;
Matches 1050; Conservative
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                                                                                   New LPB protein or its fragment for promoting bone growth, treating bone fractures, increasing or maintaining bone density, and treating osteoporosis, arthritis, sarcopenia and periodontal disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; vulnerary; bone growth; therapy; bone fracture; prophylaxis; osteoblast proliferation; osteoporosis; muscle loss; bone loss; endocrine disorder; arthritis; sarcopenia; periodontal disease; cartilage differentiation; wound healing; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
                                                                                                                                                                                                  TGTGACTGTGTGTAGAGGAAACGCAGGAGGGTAACTGCAGCCTTCGTAGCAGCAC 1254
                                                                                                                                                                                                                  TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma; graft versus-host diseases; rheumatoid arthritis; psoriasis; inflammatory bowel disease; septic shock; ulcerative colitis; crohn's disease; chronic myelogenous leukemia, cancer; liver disease; chronic myelogenous leukemia, ravior disease; cachexia, autoimmune disease; myasthemia gravis; autoimmune diabetes; systemic lupus erythematosus; transgenic animal; diagnosis; prophylatic; therapeutic; human; ds.
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Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, thematoid arthritis, psoriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis, Lyme's disease, cachexia and autoimune clisease e.g. myasthemia gravis, autoimmune diabetes and systemic ulpus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, playmentides are suitable for monitoring clinical trials. TANGO plypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2839 BP; 858 A; 532 C; 600 G; 849 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 914.2; DB 21
Pred. No. 1.7e-267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of cellular disorders can be treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 83.5%;
Matches 1050; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  538
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                                                                                                                                                                                       CAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCCTTCAGTTGAGACCAAAG 1229
                                                                                                                                                                                                       ACTGGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCACGAGGAA 1197
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 810 GTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGT 869
                                                                                                                                                                                                                                              TGTGACTGTGTGTGTAGAGGAAACGCAGGAGGGTAACTGCAGCCTTCGTAGCAGCAC 1254
                                                                                                                                                                                                                                                                                                                                                       Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
                                                        GTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAAC
                                                                                                                     ACCTTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC
                        TTCTCAGTGTCCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT
                                                                                                                                          GTGGTGAATCTGGAATCTCCTCAAGGAAGGTAAAACTCTACAGCTGCACACCCCGGAAC
                                                                                                                                                                                                                                                                                                                                          Human PRO200 nucleotide sequence.
                                                                                                                                                                                                                                                                                            AAZ34296 standard; cDNA; 2849
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98US-0077632.
98US-0077641.
98US-0077641.
98US-0077649.
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98US-0078916.
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98US-0079656.
98US-0079653.
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Chen J;

GENENTECH INC

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New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
Baker KP,
Yuan J,
                                                                                                                                                                                            2; Fig 206; 530pp; English
  Gurney A,
  Goddard A,
                                           WPI; 1999-551358/46.
P-PSDB; AAY41766.
  Wood WI,
                                                                                                                                                                                               Claim
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invention

The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33891 to AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and polypeptide sequence given in the exemplification of the present

Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

Gaps 4; Length 2849; 203; Indels Score 914.2; DB 20; Pred. No. 1.7e-267; 0; Mismatches Query Match
Best Local Similarity 83.5%;
Matches 1050; Conservative

206 266 146 177 121 61 CCCTGCGGATTCTCTGCTGCCAGAGCCCGCCAGCGCTTCCACGCGCAGCGCAGCCTTTCCC CGG----GCTGGGCTGAGCCTTGGAGTCGTCGCTTCCCCAGTGCCCGCGGGGGTGAGCC reecegreereaagagacreeggagreecreericerreeaagreecegeggager cecrecearrererecreceasasereseceseserresecereseceaseserrecee ACCTGGAGACACAGAAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGTGGAAACTA 87 62 147 122 207 9 ŏ qq ₹ ద

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<u>crcaccccacrcadccaaargagccrcrrcaggcrrcrccrccracradarcracccragcc</u>

CTCGCCCCAGTCAGCCAATGCTCCTCCTCGGCCTCCTCCTGCTGACATCT

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537 626 597 989 657

TCTAAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGATGAGTATTTTCCATCTGAACCC GGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGAACCC AGTGATGGAAGTGTTTTAGGACGCTGGTGTGGTTCTGGGACTGTGCCAGGAAAGCAGACT <u> a dergan cerana rina de de cercencia de recenera cercencia a a a capara recenera a a a capara recenera a a capara capara recenera a capara capara recenera a capara capara recenera a capara </u> 267 538 627 598

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November 26, 2003, 00:11:33 completed: Novem Search cor Job time

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Patent No. 649568
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 1999-05-03
FRICR PILING DATE: 1999-05-03
FRICR FILING DATE: 1999-11-10
FRICR FILING DATE: 1999-11-10
FRICR FILING DATE: 1999-05-04
FRICR FILING DATE: 1999-11-10
FRICR FILING DATE: 2000-02-04
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Best Local Similarity 99.4
Matches 1460; Conservative
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US-09-564-595D-34
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    US-09-564-595D-34
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                                                  2233 TTGTTTGCTTCAATAGCCTTCCCTGCAGGACTTCAAGTGTCTTCTAAAAGACCAGAGGG
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                                                                                                                                                                                                            Sequence 42, Application US/09706968

Patent No. 6528050

GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West V. James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REPERENCE: 98-60C1
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OS SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                  ACCAANAGGAGTCAATCACAAAGCACTGC 1470
                                                                                                                    2295 ACCAAGAGGAGTCAATCACAAAGCACTGC 2323
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US-09-706-968-42
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; LOCATION: (1049)...(2086)
US-09-457-066-42
        Sequence 42, Application
Patent No. 6432673
GENERAL INFORMATION:
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APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Haddington, Christopher S.
APPLICANT: Sheepard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilberson, Debra G.
APPLICANT: Gilberson, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVE
FILE REFERENCE: 98-60.
CURRENT APPLICANTON NUMBER: US/09/457,066
CURRENT PELLING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 42
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i OTHER INFORMATION:
US-09-040-220D-1
               LENGTH: 2825
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: Human
LOCATION: 2689
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APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
FILE REPERENCE: P11.2
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT APPLICATION NUMBER: US/09/040,220D
NUMBER OF SEQ ID NOS: 8
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Patent No. 6391311
GENERAL INFORMATION:
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US-09-040-220D-1
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US-09-564-595D-32
Sequence 32, Application US/09564595D
Patent No. 6495668
GENERAL INFORMATION:
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1 Sequence 1, Application US/09265686

2 Patent No. 6455283

3 GENERAL INFORMATION:

APPLICANT: Ferrara, Napoleone

APPLICANT: Kuo, Sophia S.

7 TILLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGI

FILE REPRENCE: P1122P2

CURRENT APPLICATION NUMBER: US/09/265,686

CURRENT APPLICATION NUMBER: US 09/40,220

PRIOR PILLING DATE: 1998-03-17

PRIOR PILLING DATE: 1998-03-17

PRIOR PILLING DATE: 1998-03-17

PRIOR PILLING DATE: 1998-03-17

PRIOR PILLING DATE: 1998-03-17

PRIOR PILLING DATE: 1998-03-17

PRIOR PILLING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 1

LENGTH: 2825
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Best Local Similarity 83.5%; Pred. No. 1.2e-270;
Matches 1050; Conservative 0; Mismatches 203;
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; OTHER INFORMATION: Any nucleotide
US-09-265-686-1
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Fatent No. 6528050

GENERAL INFORMATION:

APPLICANT: Hart, Charles E.

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APPLICANT: Shepard, Paul O.

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; LOCATION: (154)...(1191)
US-09-706-968-1
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ORGANISM: Homo sapiens
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Pred. No. 6.9e-260;
0; Mismatches 197; Indels
59.6%;
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Best Local Similarity 83.4
Matches 1011; Conservative
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; LOCATION: (154)...(1191)
US-09-564-595D-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                    Sequence 1, Application US/09457066
Fatent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, NGNOWTH FACTOR HOMOLOG ZVEGF3
FILE REPRENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.6%; Score 878.8; DB 4; Best Local Similarity 83.4%; Pred. No. 6.9e-260; Matches 1011; Conservative 0; Mismatches 197;
                                                                                                                                                          1201 CACCAGCAGCTC 1212
                                                                                                                         1243 TCGTAGCAGCAC 1254
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; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-457-066-1
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ORGANISM: Homo sapiens
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     AGCGCAGCCTTTCCCCGG----GCTGGGCTGAGCCTTGGAGTCGTCGCTTCCCCAGTGCC
                                                                                                         AGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGACTCGGGAGTCGCTGCTTCCAAAGTGCC
                                                                                                                                         CGCCGCGAGTGAGCCCTCGCCCCAGTCAGCCAAATGCTCCTCCTCGGCTCCTCCTGCTG
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                                                                                                                  Length 1095
                                                                                                                                              Indels
                                                                                                                                            0; Mismatches 157;
                                                                                                                Score 745.8; DB 4;
Pred. No. 4e-219;
                                                                                                               Query Match
Best Local Similarity 84.3%;
Matches 840; Conservative
                                                                   ; OTHER INFORMATION: Fused DNA
US-09-457-066-50
                           TYPE: DNA
ORGANISM: Artificial
FEATURE:
  SEQ ID NO 50
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                                            TITCCTICTGAACCAGGGITCIGCAICCACTACAACAITGICAIGCCACAAITCACAGAA
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Fatent No. 6432673
GENERAL INFORMATION:
APPLICANT: GAO.
APPLICANT: Bart, Charles E.
APPLICANT: Sheppard, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVER:
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-457-066-50
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1016 GTCTCCTGGTCAAGCGCTGTGGAGGAAATTGTGCCTGTTGTCCCATAATTGCAATGAAT 1075
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740 gagriggriggarcrigaaccrircraacagaggaggraagarraracaggcrigcacaccrigra 799
                                                                                                                                                                                                                                                                                                                                                                                                                  800 ACTICICAGIGICCATAAGGGAAGAACTAAAGAGAACCGATACCATITICIGGCCAGGIT 859
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                                                                          776 GTACCTTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACA 835
                                                                                                         896 AAGIGGIGAAICIGAAICICCICCAAGGAAGAGGIAAAACICIACAGCIGCACACCCCGGA
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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Bridhington, Christopher S.
APPLICANT: Sheppard, Rimberly E.
APPLICANT: Shoemaker, Rimberly E.
APPLICANT: Gamesker, Mimberly E.
APPLICANT: Gamesker, James W.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF3
FILE REFERENCE: 98-60 MOMBER: US/09/457,066
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT APPLICATION NUMBER: US/09/457,066
SOFTWARE: FastESQ for Windows Version 3.0
SOFTWARE: FastESQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: misc_feature

) LCCATION: (1)...(1035)

) OTHER INFORMATION: n = A,T,C or G

US-09-457-066-6
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Patent No. 6432673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAAATTCCAGTTTTCCA 139
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Best Local Similarity 84.3%; Pred. No. 4e-219;
Matches 840; Conservative 0; Mismatches 157; Indels 0;
                                                                                                         1040 AGTGTGACTGTGTGCAGAGGAGGAGCACAGGAGGATA 1076
                                                                                 1196 AATGTGACTGTGTGTGTAGAGGAAACGCAGGAGGGTA 1232
                                                                                                                                                                                                                                                                                                                        APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-6001
CURRENT PPLICATION NUMBER: US/09/706,968
CURRENT PILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                     sequence 50, Application US/09706968; Patent No. 6528050; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                          RESULT 10
US-09-706-968-50
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                                    Query Match 44.8%; Score 660.8; DB 4; Length 1035; Best Local Similarity 52.9%; Pred. No. 5.4e-193; Matches 547; Conservative 250; Mismatches 237; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and OTHER INFORMATION: 2
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FEATURE:
OTHER INFORMATION: degenerate sequence derived from SEQ ID NOS: 1 and
OTHER INFORMATION: 2
Sequence 6, Application US/09706968
Patent No. 6528050
GRNERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shemensker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVI
FILE REFERENCE: 98-601.
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR PILING DATE: 2000-13-11
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FSSESEQ for Windows Version 3.0
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NO 6
SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc_feature
) LOCATION: (1)...(1035)
) OTHER INFORMATION: n = A,T,C or
US-09-706-968-6
                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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240 300 CGGGCTGAGTCCAACCTGAGCAAGTTGCAGCTCTCCAGCGACAAGGAACAGAACGGA 315 GTGCAAGATCCCCGGCATGAGAGGTTGTCACTATATCTGGTAATGGGAGCATCCACAGC 375 GATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGCTGGAAGATCCAGAA 495 420 480 9 ||:||:||:||:||:||:||:||:||:||:||:|| ||:|| ||:|| ||:|| ||:|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| ||::|| CCGAAGTITCCTCATACGTACCAAGAAATATGGTGCTGGTGGGGGAGATTAGTTGCAGTA GACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCCAGTGATGGAAGTGTTTTA GGACGCTGGTGTGTTCTGGGACTGTGCCAGGAAAGCAGACTTCTAAAGGAAATCATATC AGTATTATCATGCCACAAGTCACAGAAACCACGAGTCCTTCGGTGTTGCCCCCTTCATCT TIGICATIGGACCIGCICAACAAIGCIGIGACIGCCITCAGIACCITGGAAGAGCIGATI ö Length 1035; Indels Query Match
44.8%; Score 660.8; DB 4;
Best Local Similarity 52.9%; Pred. No. 5.4e-193;
Matches 547; Conservative 250; Mismatches 237; 736 8

RESULT 12 US-09-706-968-6

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880 TATGGGAAAAAAAGCAAAGTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTAC 939
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337 AGAGTTGTCACTATATCTGGTAATGGGAGCATCCACAGCCCGAAGTTTCCTCATACGTAC 396
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Sequence 6, Application US/09564595D
Setent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-04
SPIOR FILING DATE: 1999-06-04
SPIOR FILING DATE: 1900-02-04
SOFTWARE FEATON NUMBER: US 60/180,169
SPIOR FILING DATE: 2000-02-04
SOFTWARE FACTOR NUMBER: US 60/180,169
SPIOR FILING DATE: 2000-02-04
SOFTWARE FACTOR NUMBER: US 60/180,169
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US-09-564-595D-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :: ||:|| || :| ||:|| ::: || :|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
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940 AGCTGCACACCCCGGAACTTCTCAGTGTCCATACGGGAAGAGCTAAAGAGAGACAGATACC 999
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APPLICANT: Gilbertson, Debra G.
APPLICANT: Hart, Charles B.
IIILE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
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Page 12

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US-09-564-595D-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    899 TGGTGAATCTGAATCTCCTCAAGGAAGGTAAAACTCTACAGCTGCACACCCCGGAACT 958
                                                                                                                                                                                                                                                                                                                                                                                                                                      356 GTAATGGGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAAGAAATATGGTGCTGG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                590 AGCAGACTTCTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCAT 649
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                                                                                                                                                                                                                                                                                                                                                 9.3%; Score 137.2; DB 4; Length 1472; 52.5%; Pred. No. 6.7e-32; Live 0; Mismatches 373; Indels 75;
TITLE OF INVENTION: LICAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
EARLIER APPLICATION NUMBER: US 60/180,169
EARLIER FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                               Matches 496; Conservative
                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
) LOCATION: (93)...(1205)
US-09-540-224-3
                                                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
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LENGTH: 1472
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1134 ----AAAAACTGGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACC 1189
1079 AGTGTGTCCCACGTAAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACC---- 1133
                                                                      1042 CATGCAGCTCAGGGAAGACAGTGAAGTATCATGAGGTATTGAAGTTTGAGCCTGGAC 1101
                                                                                                                                                                                                                      1102 ATTTCAAGAGAAGGGCAAAGCTAAGAAAATGGCTCTTGTTGATATCCAGCTGGATCATC 1161
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                                                                                                                                                                                                                                                                                                    1190 ACGAGGAATGTGACTGTGTGTAGAGGAAACGCAGGAGGGTAA 1233
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APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US 09/304,216
PRIOR PILING DATE: 1999-05-03
PRIOR PILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR PILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 52, Application US/09564595D
; Patent No. 6495668
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; LOCATION: (93)
US-09-564-595D-52
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1079 AGTGTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACC---- 1133
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                                                                                                                                                                                                                                                                                                                                                                                                1102 ATTTCAAGAGAAGAGGAGAAAGCTAAGAATATGGCTCTTGTTGATATCCAGCTGGATCATC 1161
                                                                                                                                                                                                             959 TCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGTC 1018
                                                                                                                                                                                                                                                                1042 CATGCAGCTCAGGGAAGACAGTGAAGAAGTATCATGAGGTATTGAAGTTTGAGCCTGGAC 1101
                      688 CAATAACGGACCCCACTCTCACTGCTGATGCCCTGGGACAAAACTGTCGCAGAATTCGATA 747
                                                  CCTTGGAAGAGTGATTGGTACTAGAGCCAGATGGAGAGGTGGACTTGGACAGCC 838
                                                                        148 CCGTGGAAGATCTAACTTAAGCACTTCAATCCAGTGTCTTGGCAAGATGATCTGGAGAATT 807
                                                                                                     839 TCTACAAGCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAAG 898
                                                                                                                                861
                                                                                                                                                         899 TGGTGAATCTCGTCAAGGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAACT 958
                                                                                                                                                                           922 ACTCTGTGAACTCAGGAAGAGCTGAAGCTAACCAATGCAAGTCTTCTTCCCACGATGCC 981
-----CICAACAAIGCIGIGACIGCCIICAGIA 778
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Search completed: November 26, 2003, 05:52:23 Job time : 77.0009 secs

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NAME/KEY: unsure
LOCATION: (1447)
OTHER INFORMATION: can be a, c, g or
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Sequence 6, Appli
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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APPLICANT: LEE, Xuri
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: GESTWAN, Anne
APPLICANT: BESTRAULZ, Christer
TITLE OF INVENTION: PLATELE-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELE-DERIVED
TITLE OF INVENTION: PLATELE-DERIVED
TITLE OF INVENTION: PLATELE-DERIVED
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TITLE OF INVENTION: PLATELE-DERIVED
TITLE OF INVENTION UNMERR: 09/410,349
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR PILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-03
PRIOR PLILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/135,426
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PLILING DATE: 1999-07-15
PRIOR PLILING DATE: 1999-07-15
PRIOR PLILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: 60/144,022
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US-09-998-833A-487

US-09-918-15A-487

US-09-918-585A-487

US-09-978-423A-487

US-09-978-423A-487

US-09-978-133A-487

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US-10-140-018-285

US-10-140-018-285

US-10-140-922-285

US-10-141-698-285

US-10-141-702-285

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US-10-141-702-285
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Patent No. US2002164687A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
      \begin{array}{c} 6 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 \ 0.05 
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                    CTGGTCAAGCGCTGTGGAAGAAATTGTGCCTGTTGTCTCCATAATTGCAATGTCAG
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| Sequence 6, Application US/10131600
| Publication No. US20030082670A1
| CENERAL INFORMATION:
| APPLICANT: BRIKSSON, U1f
| APPLICANT: ALTS. Xuri
| APPLICANT: ALTRALO, Kari
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| APPLICANT: ALTRALO, Kari
| APPLICANT: HELDIN Carl-Henrik
| APPLICANT: ALTRALO, Auxi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Sequence 3, Application US/09823033 | Patent No. US20020004225A1 | Patent No. US20020004225A1 | GENERAL INFORMATION: APPLICANT: Hart, Charles E. APPLICANT: Glibertson, Debra G. TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE, ITLE OF INVENTION: LIGAMENT AND CARTILAGE | FILE REFERENCE: 00-12 | CURRENT APPLICATION NUMBER: US/09/823,033 | CURRENT FILING DATE: 2001-03-29 | NUMBER OF SEQ ID NOS: 5 | SOFTWARE: FastSEQ for Windows Version 3.0 | SEC ID NOS: 5 | SOFTWARE: FastSEQ for Windows Version 3.0 | SEC ID NOS: 5 | SOFTWARE: FastSEQ for Windows Version 3.0 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | SEC ID NOS: 5 | S
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99.9%; Score 1473; D
Best Local Similarity 100.0%; Pred. No. 0;
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; LOCATION: (1447); OTHER INFORMATION: can be a, US-10-131-600-6
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182 C-GGCTGGGCTTGGAGTCGTCGTCCTCGGTGCCCGCGGGGGGGCCTCG 1034 182 CCCCAGTCAGCCTCTCCTCGGCCTCTCTGCTGACATCTGCCCTGGCGGCC 24	1275 GATTAGTTGCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAATTTGGGC 481	1515 TCTGCATCCACTACAGGATTATCATGCCACAAGTCACAGAACCACAGAACCTTCGGTGT 1574 722 TGCCCCTTCATCTTTGTCATTGCCCTCACAATGCTGTGACTCCTTCAGGATCCTTCAGGACTCCTTCAGGACTCCTTCAGGACTCCTTCAGGACTCCTTCAGGACTCATCAGGACTCGTTCAGGACTCGTTCAGGACTCGTTCAGGACTCGTTCAGGACTTCAGGACTTCAGGACTTCGTTCAGGACTTGGACTTCGGTACTTGGACAGCCTT 841 1635 TGGAAGACGATTCGGTACCTAGAGCCAGGTCGATGGCAGGAGACAGCCTCT 841 1635 TGGAAGACGATTTGGGCAAGAGCCAGGTTTCCTGATGGCAGAAAAAAAA	

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                                                                                                                          Sequence 3, Application US/10264361
Fublication No. US20030087870A1
GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
TITLE REFERENCE: 00-53
CURRENT FILING DATE: 2002-10-03
FILE REPLICATION NUMBER: US/10/264,361
CURRENT FILING DATE: 2002-10-03
FRICR FILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
                Query Match 98.0%; Score 1444.8; Best Local Similarity 99.4%; Pred. No. 0; Matches 1460; Conservative 0; Mismatches
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; LOCATION: (1049)...(2086)
US-10-264-361-3
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US-10-264-361-3
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Best Local Similarity 83.5%; Pred. No. 4.6e-296;
Matches 1050; Conservative 0; Mismatches 203;
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/184,216
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 1
LENGTH: 2825
TWEND 1
                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FBATURE:
NAME/KEY: misc feature
LOCATION: (2689)..(2689)
OTHER INFORWATION: Any nucleotide
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US-10-178-442-1
| Sequence 1, Application US/10178442
| Sequence 1, Application No. US20030113870A1
| Publication No. US20030113870A1
| GENERAL INFORMATION:
| APPLICANT: Ferrara, Napoleone
| APPLICANT: Kuo, Sophia 8
| TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
| FILE REFERENCE: 11669.112USD2
| CURRENT APPLICATION NUMBER: US/10/178,442
| CURRENT FILING DATE: 2002-09-24
| PRIOR APPLICATION NUMBER: US 09/265,686
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PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR PILLING DATE: 1999-12-25
PRIOR FILING DATE: 2000-02-25
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-05-14
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 2000-06-29
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; LOCATION: (288)...(1322)
US-09-796-753-5
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ORGANISM: Homo sapiens
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        778 ACCTIGGAAGAGCTGATICGGTACCTAGAGCCAGATCGAIGGCAGGTGGACTTGGACAGC 837
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TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILLE REFERENCE: 7853.227-929

CURRENT APPLICATION NUMBER: US/09/796,753

CURRENT FILING DATE: 2001-03-01
PRIOR PILING DATE: 1998-10-30

PRIOR PILING DATE: 1998-10-30

PRIOR PILING DATE: 1998-12-30

PRIOR PILING DATE: 1999-02-26

PRIOR PILING DATE: 1999-02-26

PRIOR PILING DATE: 1999-02-26

PRIOR PILING DATE: 1999-02-14

PRIOR PILING DATE: 1999-02-14

PRIOR PILING DATE: 1999-06-18

PRIOR PILING DATE: 1999-06-18

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FILING DATE: 1999-09-30
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FILING DATE: 1999-12-29
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Sequence 5, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC11
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   Paoni, Nicholas F.
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Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
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Gerritsen, Mary E.
Goddard, Audrey
Goddward, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Bllen
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AGTGATGGAACTATATAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAAACAGATT 686
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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Patent No. US20020169284A1
GENERAL INFORMATION:
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Gerritsen, Mary E.
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Filvaroff, Ellen
Fong, Sherman
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Botstein, David
Desnoyers, Luc
Eaton, Dan
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APPLICANT: ROY MAYERARCA AND APPLICANT: SRetton, David L. APPLICANT: SRetton, David L. APPLICANT: SRetton, David L. APPLICANT: STREAM STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRAIGHT STRA
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R APPLICATION NUMBER: 60/082568
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R APPLICATION NUMBER: 60/083322
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R APPLICATION NUMBER: 60/081195

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APPLICATION UNDER: 60/083742
FILING DATE: 1998-04-30
APPLICATION NUMBER: 60/084366
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APPLICATION NUMBER: 60/084637
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APPLICATION NUMBER: 60/08441
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APPLICATION NUMBER: 60/082804
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             PRIOR PILING DATE: 1998-05-07
PRIOR PELING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
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538 AGTGATGGAAGTGTTTTAGGACGCTGGTGTGTTCTGGGACTGTGCCAGGAAAGCAGACT 597

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1047 TTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGT 1106
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                   627 AGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAGGAAACAGATT 686
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Godowski, Paul'J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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Patent No. US20020177553A1
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Goddard, Audrey
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Desnoyers, Luc
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APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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APPLICANT: Reonly, Micholas F. F. APPLICANT: Reonly, Micholas F. APPLICANT: Replicant: Behalton: Behalton: Behalton: Behalton: Parallel Micholas F. APPLICANT: Behalton: David I. APPLICANT: Replicant: Behalton: David I. APPLICANT: Replicant: Behalton: David I. APPLICANT: William I. APPLICANT: William P. Miccogneric III and the INVARITON: Abids Encoding the Same Intime Der INVARITON: Abids Encoding the Same Intime Der INVARITON: Abids Encoding the Same Intime Der INVARITON: Abids Encoding the Same Intime Der Intime Der INVARITON: Abids Encoding the Same Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Intime Der Int
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APPLICATION NUMBER: 60/080334
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122 CGG----GCTGGGCTGAGCCTTGGAGTCGTCGCTTCCCCAGTGCCCGCGCGAGTGAGCC 177 CTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGCTGACATCTGCCCTGGCC 326 446 CCCTGCGATTCTCTGCCTGCCAGAGCCGGCCAGGCGCTTCCACCGCAGCGCGTTTCCC 121 207 rescentericaranacacacrecedacrescrecricerandrescesses 266 327 GGCCAGAGACAGGGGACTCAGGCGAATCCAACCTGAGTAGTAATTCCAGTTTTCCAGC 386 298 GACAAGGAACAGAACGGAGTGCAAGATCCCCGGCATGAGAGAGTTGTCACTATATCTGGT 357 538 AGTGATGGAAGTGTTTTAGGACGCTGGTGTGTTCTGGGACTGTGCCAGGAAAGCAGACT 597 238 GGCCAAAGAACGGGGACTCGGGCTGAGTCCAACCTGAGCAGCAAGTTGCAGCTCTCCAGC 2 ACCTGGAGACACAGAAGAGGGCTCTAGGAAAATTTTGGATGGGGATTATGTGGAAACTA 147 CCCTGCGATTCTCTGCTGCCTGGCTCGGCGCTTCCACCCCAGTGCATCCTCCC CTCGCCCCAGTCAGCCAAATGCTCCTCCTCGCCTCCTGCTGACATCTGCCCTGGCC 358 AATGGGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAAGAAATATGGTGCTGGTG 418 TGGAGATTAGTTGCAGTAGATGAGAATGTGCGGATCCAGCTGACATTTGATGAGAGATTT 567 GGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAACCC 478 GGGCTGGAAGATCCAGAAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCC Gaps 4 Length 2849; 62.0%; Score 914.2; DB 10; Length 83.5%; Pred. No. 4.6e-296; ive 0; Mismatches 203; Indels R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/084643

R FILING DATE: 1998-05-07

R APPLICATION NUMBER: 60/08539

R FILING DATE: 1998-05-13

R FILING DATE: 1998-05-13

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R APPLICATION NUMBER: 60/085328

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R APPLICATION NUMBER: 60/085573

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R APPLICATION NUMBER: 60/085697 FILING DATE: 1998-05-07
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084600 FILING DATE: 1998-05-15
APPLICATION UNDBER: 60/085579
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085580 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084627 APPLICATION NUMBER: 60/085700 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085689 Query Match 62.0 Best Local Similarity 83.5 Matches 1050; Conservative 267 62 178 PRIOR à ð ద ઠે d ò 셤 ò 셤 ò 셤 ò g à 셤

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same
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CURRENT APPLICATION NUMBER: US/09/99,832A
CURRENT FILING DATE: 2001-10-24
FRIOR FILING DATE: 2001-10-24
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                       Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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GGATTCTGCATCCACTACAGTATTATCATGCCACAAGTCCACAGAAACCACGAGTCCTTCG
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                                                                                                                                                                                                                                                                                      Sequence 487, Application US/0999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Bestein, David
APPLICANT: Bestein, David
APPLICANT: Eaton, David
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Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Grimaldi, J. Christopher
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Hillan, Kenneth J.
Kljavin, Ivar J.
Kujavin, Ivar J.
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Napier, Mary A.
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                                                            687 TCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTTCCTTCTGAACCA 746
                                                                                                  658 GGATTCTGCATCCACTACAGTATTATCATGCCACAAGTCACAGAAACCACGAGTCCTTCG 717
                                                                                                                      147 GGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCA 806
                                                                                                                                                         GIGITGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACAATGCTGTGACTGCCTTCAGT 777
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddwski, Mary E.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 487, Application US/09978608A; Publication No. US20030045462A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ferrara, Napoleon
Filvaroff, Ellen
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Desnoyers, Luc
Eaton, Dan
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Pan, James;
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US-09-978-608A-487
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                                                                                                                                                                                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630PLC22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 487
LENGTH: 2849
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; NAME/KET: unsure
; LOCATION: 2715
; OTHER INFORMATION: unknown base
US-09-978-608A-487
                          Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                      Williams, P. Mickey Wood, William I.
Paoni, Nicholas F
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ORGANISM: Homo sapiens
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ACCTTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGGC 837
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                                                                             807 GTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGT 866
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Botstein, David
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Eaton, Dan
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; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 487
; LENGTH: 2849
                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: unknown base US-09-978-585A-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1050; Conservative
                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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867 ACCTIGGAAGACCITATICGAIAICTIGAACCAGAGAGATGGAGATGACTIAGAAGAI 926
                                                                                    CTCTACAAGCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAA 897
                                                                                                                GTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAAC 957
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                  958 ITCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT
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CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
FRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 1997-10-17
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kujavin, Ivar J.
Kujevin, Mary A.
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Shelton, David L.
Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Paoni, Nicholas F.
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Filvaroff, Ellen
Fong, Sherman
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Botstein, David
Desnoyers, Luc
Baton, Dan
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R APPLICATION NUMBER: 60/080154

DR APPLICATION NUMBER: 60/080134

R PILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080328

R FILING DATE: 1998-04-01

DR APPLICATION NUMBER: 60/080338

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R APPLICATION NUMBER: 60/078936
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R APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
                                    FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
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APPLICATION WINBER: 60/06364
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APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/077632
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APPLICATION NUMBER: 60/077641
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APPLICATION NUMBER: 60/078004
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APPLICATION NUMBER: 60/078886
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APPLICATION NUMBER: 60/079689
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APPLICATION WINBER: 60/079663
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APPLICATION NUMBER: 60/079728
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APPLICATION NUMBER: 60/081203
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R FILING DATE: 1998-04-29

R APPLICATION NUMBER: 60/083558

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R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/081838
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R APPLICATION NUMBER: 60/083392
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R APPLICATION NUMBER: 60/082804
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R APPLICATION NUMBER: 60/082796
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APPLICATION NUMBER: 60/081817
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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APPLICATION NUMBER: 60/085323
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                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 62.0%; Score 914.2; DB 11; Length 2849; Best Local Similarity 83.5%; Pred. No. 4.6e-296; Aatches 1050; Conservative 0; Mismatches 203: ThAple 4.
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR PAPELICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/085573
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
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778 ACCTTGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGC 837

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ସ୍ଥ	867 ACCTIGGAAGACCITATICGATATCTIGAACCAGAGAGAIGGCAGTIGGACTIAGAAGAI	VT 926
δ	838 CTCTACAAGCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAAA	AA 897
qq	927 CTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTTGGAAGAAAATCCAGA	j 3A 986
λõ	898 GTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACAGCTGCACACCCCGGGAAC	AC 957
qq	987 GIGGIGGATCTGTAACAGAGGAGGTAAGATTATACAGCTGCACACCTGTAAA	1 1046
ò	958 TICTCAGIGICCATACGGGAAGAGCTAAAGAGGACAGATACCATATICTGGCCAGGITGI	37 1017
qq	1047 TTCTCAGTGTCCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGT	J 1106
λŏ	1018 CTCCTGGTCAAGCGCTGTGGAAGATTGTGCCTGTTGTCTCCATAATTGCAATGATGT	3T 1077
QQ	1107 CTCCTGGTTAAACGCTGTGGGGAACTGTGCCTGTTGTTCTCCAAATGCAATGTATGT	JT 1166
δλ	1078 CAGTGTCCCACGTRARGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAA	AA 1137
qa	1167 CANTGITCTCCAAGGAAAGTTACTAAAAATACCACGAGGTCCTTCAGTTGAGACGAAAG	AG 1226
οy	1138 ACTGGAGTCAAAGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCCACGAGGAA	AA 1197
qq	1227 ACCGGTGTCAGGGGATTGCACAAATCACTCACGGAGGCCCTGGAGGAGCACGAGGAGA	kG 1286
δ	1198 TGTGACTGTGTGTAGAAAACGCAGGAGGGTAACTGCAGCCTTCGTAGCAGCC	1254
ДД	1287 IGHTHITHITHICAGAGGGGGGCACAGGAGGATAGCCGCATCACCACCAGCAGCTC	1343
Search co	Search completed: November 26, 2003, 09:32:33	

Search completed: November 26, 2003, 09:32:33: Job time : 366.884 secs

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Reg
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15537.553 Million cell updates/sec
                                                                                                                                                                                                                          November 25, 2003, 23:55:21 ; Search time 3146.15 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 cacctggagacacagaagag......aatcacaaagcactgcaccg 1474
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1: \cgm2 \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) \( \) 
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY NUC Gapoxt 1.0
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Maximum DB seg length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                            Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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44: / cgp2_6/ptodata/2/pna/US10bb_coMB_seq: 45: / cgp2_6/ptodata/2/pna/US10bb_coMB_seq: 45: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 47: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 47: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2/pna/US10la_coMB_seq: 49: / cgp2_6/ptodata/2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ssult No.	Score	% Query Match	% Query Match Length DB ID	DB	ID	Description	
	1473	99.8	1474	; -	1 1473 99,9 1474 1 PCT-US99-22668-6	Sequence 6, Appli	i Idc
7	1473	99.9	1474	0	PCT-US99-22668-6	Sequence 6, Appli	p)
e	1473	99.6	1474	21	US-09-410-349A-6	Sequence 6, A	App]
4	1473		1474	r.	11S-09-852-209-6	Semience 6. A	200

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Sequence 11108, A Sequence 11108, A Sequence 11108, A Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 9339, Ap Sequence 9339, Ap Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 285, App Sequence 1, Appli Sequence 1, Appli Sequence 287, App Sequence 287, App Sequence 287, App Sequence 1, Appli Sequence 1, Appli Sequence 287, App Sequence 287, App Sequence 287, App Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence 287, Appli Sequence
                                                              42, Appl
3, Appli
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Sequence 487,
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Sequence 42
Sequence 3,
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Sequence 3,
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                              Sequence
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Sequence 6, Application PC/TUS9922668B
GENERAL INFORMATION:
APPLICANT: LUUDMIG INSTITUTE FOR CANCER RESEARCH
APPLICANT: LUUDMIG INSTITUTE FOR CANCER RESEARCH
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
FILE OF INVENTION: THEREFOR, AND USES THEREOF
FURRENT PRILING DATE: 1999-09-30
CURRENT FILING DATE: 1999-09-30
EARLIER APPLICATION NUMBER: 60/102,461
EARLIER APPLICATION NUMBER: 60/108,109
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-11-2
EARLIER FILING DATE: 1998-11-2
EARLIER FILING DATE: 1998-12-18
EARLIER FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 60/113,002
EARLIER APPLICATION NUMBER: 60/113,002
EARLIER APPLICATION NUMBER: 60/113,426
EARLIER APPLICATION NUMBER: 60/113,426
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARER: PALICATION NUMBER: 60/144,022
EARLIER FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARER: PALICATION NUMBER: 60/144,022
EARLIER FILING DATE: 1999-07-15
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EARLIER FILING DATE: 1099-07-15
                                       US-09-540-703-3

US-09-540-703-3

US-09-541-752-42

US-09-765-121-3

US-09-823-03-3

US-09-823-03-3

US-10-139-583-42

US-10-139-583-42

US-10-144-771-11108

US-09-304-216-3

US-09-184-216-1

US-09-184-216-1

US-09-184-216-1

US-09-184-216-1

US-09-184-216-1

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US-09-599-596-1

US-09-291-184-87

US-09-378-188-487

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Matches 1474; Conservative 0; Mismatches
; TYPE: DNA

; ORGANISM: Murinae gen. sp.;

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1447)

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DNA CODING
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APPLICANT: LUNGIG INSTITUTE FOR CANCER RESEARCH
APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.
TITLE OF INVENTION: PLATER-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATEREPOR, AND USES THEREOF
FILE REFERENCE: PCT/US99/22669B
CURRENT PAPLICATION NUMBER: PCT/US99/22668B
CURRENT FILING DATE: 1999-09-30
EARLIER APPLICATION NUMBER: 60/102,461
EARLIER APPLICATION NUMBER: 60/102,461
EARLIER APPLICATION NUMBER: 60/103,002
EARLIER APPLICATION NUMBER: 60/110,749
EARLIER PILING DATE: 1998-11-13
EARLIER FILING DATE: 1998-12-13
EARLIER FILING DATE: 1998-12-13
EARLIER APPLICATION NUMBER: 60/113,002
EARLIER FILING DATE: 1999-12-13
EARLIER APPLICATION NUMBER: 60/113,002
EARLIER APPLICATION NUMBER: 60/113,022
EARLIER APPLICATION NUMBER: 60/113,022
EARLIER APPLICATION NUMBER: 60/114,022
EARLIER FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
COUNTAINSE: DATE: 1999-07-15
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OTHER INFORMATION: a, c, g or t
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SEQ ID NO 6
LENGTH: 1474
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FEATURE:
NAME/KEY: unsure
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Query Match
99.9%; Score 1473; D)
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches
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1141 GGAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCCACGAGGAATGT 1200
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JOS-09-1410-349A-5

GENUERL INFORMATION:
JAPPLICANT: BRIKSSON, U1f

APPLICANT: BRIKSSON, U1f

APPLICANT: BESE, Karin

APPLICANT: POWIEN, Annica

APPLICANT: FONTEN, Annica

APPLICANT: UGELA, Marko

APPLICANT: GESTMAN, Arne

APPLICANT: HELDIN, Carl-Henrik

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APPLICANT: HELDIN, Carl-Henrik

APPLICANT: 1999-10-12

CURRENT APPLICATION NUMBER: 60/100, 749

PRIOR FILING DATE: 1998-11-03

PRIOR PILING DATE: 1998-12-03

PRIOR PILING DATE: 1998-12-03

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CIHER INFORMATION: can be a, US-09-410-349A-6
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Matches 1474; Conservative 0; Mismatches
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Query Match
99.9%; Score 1473; DB 35; Length 1474;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1474; Conservative 0; Mismatches 0; IndelB 0;
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**CORMATION:

T: ERIKSSON, Ulf

T: AASE, Karin

AT: AASE, Xuri

ANT: POWTEN, Annica

**ANT: POWTEN, Annica

ANT: POWTEN, Annica

ANT: POWTEN, Annica

ANT: POWTEN, Annica

ANT: POSTWAN, Arne

**LICANT: BELDIN, CAL'Henrik

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**TILE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR

**TILE OF INVENTION: 1998-09-30

**PRIOR FILING DATE: 1998-09-11

**PRIOR FILING DATE: 1998-05-21

**PRIOR FILING DATE: 1998-07-15

**NUMBER OF SEQ ID NOS: 39

**TILE OF INVENTION NUMBER: 60/144,022

**TILE OF INVENTION OF SEQ ID NOS: 39

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    Best Local Similarity 100.0%;
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: BASE, Karin

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APPLICANT: DASE, Karin

APPLICANT: DASE, Karin

APPLICANT: DATEA, Marko

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CURRENT FILING DATE: 1999-09-30

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1999-07-15

PRIOR FILING DATE: 1999-07-15

PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PATCATION NUMBER: 60/113,002

PRIOR FILING DATE: 1999-07-15

SEQ ID NO 6

LEAGTH: 1474

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LEAGTH: 1474
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LOCATION: (1447)
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APPLICANT: AASE, Xuri
APPLICANT: BONTEN, Annica
APPLICANT: DONTEN, Annica
APPLICANT: UUTELA, Marko
APPLICANT: UUTELA, Marko
APPLICANT: OESTMAN, Arne
APPLICANT: OESTMAN, Arne
APPLICANT: BELDIN, Carl-Henrik
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APPLICANT: BELDIN, Carl-Henrik
APPLICANT: BESTSHOLTZ, Christer
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PRIOR PILING DATE: 1999-109-30
PRIOR PILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR PILING DATE: 1998-12-16
PRIOR PILING DATE: 1998-12-16
PRIOR PILING DATE: 1999-05-21
PRIOR PILING DATE: 1999-05-21
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US-10-131-600-6
Sequence 6, Application US/10131600
GENERAL INFORMATION:
APPLICANT: ERIKSSON UIF
APPLICANT: AASE, Karin
APPLICANT: PEE, Xuri
APPLICANT: PONTEN, Annica
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1081 TOTATCCACATAAATHACAAAAAACAACAACATCAAAAAAACATCAAAAAAAA
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                                        2235 TIGITIGCTICAATAGCCTICCCCGAGGACTICAAGTGTCTTCTAAAAGACCAGAGGC 2294
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                       TTGTTTGCTTCAATAGCCTTCCCCTGCAGGACTTCAAGTGTCTTCTAAAAGACCAGAGGC 1441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.0%; Score 1444.8; DB 24; Length 3571; Best Local Similarity 99.4%; Pred. No. 0; Marches 1460; Conservative 0; Mismatches 8; Indels 1; (
                                                                                                                                                                                    Sequence 42, Application US/09541752
; General InPROMATION:
; APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles B.
; APPLICANT: Briddington, Christopher S.
; APPLICANT: Sheepard, Paul O.
; APPLICANT: Sheepard, Paul O.
; APPLICANT: Sheepard, Paul O.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF9
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF9
; CURRENT FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 3.0
; SECTIVANT: SET.
                                                                                           1442 ACCAANAGGAGTCAATCACAAAGCACTGC 1470
                                                                                                         2295 ACCAAGAGGAGTCAATCACAAAGCACTGC 2323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-541-752-42
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US-09-541-752-42
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542 ATGGAAGTGTTTTAGGACGCTGGTGGTTCTGGGACTGTGCCAGGAAAGCAGACTTCTA
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                                                                                                      1695 ACAAGCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAAGCAAAGTGG 1754
1635 TGGAAGAGCTGATTCGGTACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCT 1694
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                                                                                                                                               CAGTGTCCATACGGGAAAGAGCTAAAGAGACAGATACCATATTCTGGCCAGGTTGTCTCC
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                                                                                       TGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAACTTCT
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APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 3571
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US-09-706-968-42
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                                                                                                                                                                                                                                                          Gaps
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            METHOD OF TREATING FIBROSIS
                                                                                                                                                                                                                               Score 1444.8;
Pred. No. 0;
0; Mismatches
             TITLE OF INVENTION: METHOD OF TREATING FIB FILE REPRENCE: 00-53 CURRENT APPLICATION NUMBER: US/09/695,121 CURRENT FILING DATE: 2000-10-23 NUMBER OF SEQ ID NOS: 18 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 LENGTH: 3571
                                                                                                                                                                                                                                98.0%;
                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.4*
Matches 1460; Conservative
                                                                                                                                                         FEATURE:
NAMB/KEY: CDS
LOCATION: (1049)...(2086)
US-09-695-121-3
                                                                                                                                TYPE: DNA
ORGANISM: Mus musculus
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; GENERAL INFORMATION:
; APPLICANT: Hart, Charles E.;
APPLICANT: Gilbertson, Debra G.
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; TITLE OF INVENTION: LIGAMENT AND CARTILAGE
; FILE REPREMENT 8.00-12
; CURRENT APPLICATION NUMBER: US/09/823,033
; CURRENT FILING DATE: 2001-03-29
; NUMBER: OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
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; FRATURE:
; NAME/KEY: CDS
; LOCATION: (1049) ... (2086)
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                                                            Query Match
Best Local Similarity 99.4
Matches 1460; Conservative
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Db 2115 CACTGGCATTCTGTGTACCCCACAAGCAACCTTCATCCCCACCAGGGTTGGCCGCAGGG 2174	Qy 1322 CTCTCAGCTGCTGATGCTAGGTAAAGATCTTACTCGTCTCCCAACCAA	1382 TIGITIGCITCAAIAGCCITCCCCTGCAGC	OY 1442 ACCAANAGAGTCAATCACATGC 1470 Db 2295 ACCAAGAGGAGTCAATCACAAAGCACTGC 2323	RESULT 13 US-10-139-583-42 ; Sequence 42, Application US/10139583	; GENERAL INFORMATION: ; APPLICANT: Gao, Zeren ; APPLICANT: Hart, Charles E. ; APPLICANT: Piddington, Christopher S.		; TITLE OF INVESTION: GROWTH FACTOR HOMOLOG ZVEGF3; PILE REFERENCE: 98-601, 139,583; CURRENT APPLICATION NUMBER: US/10/139,583; CURRENT FILING DATE: 2002-05-02	; PKIOR APPLICATION NUMBER: 09/457,066 ; NUMBER OF SEQ ID NOS: 50 ; SOFTWARE: FastSEQ for Windows Version 3.0	; SEQ ID NO 42 ; LENGTH: 3571 ; TYPE: DNA ; ORGANISM: Mus musculus	; FRATURE: ; NAME/KEY: CDS ; LOCATION: (1049)(2086) US-10-139-583-42	Query Match 98.0%; Score 1444.8; DB 46; Length 3571; Best Local Similarity 99.4%; Pred. No. 0; Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1;	Qy 2 ACCTGGAGACACAGAAGGGCTCTAGGAAAATTTTGGATGGGGATTATGTGGAAACTA 61 Db 856 AACTGGAGACACAGAAGGGCTCTAGGAAAAACTTTTGGATGGGATTATGTGGAAACTA 915	Qy 62 CCTGGGATTCTCTGCTGCCAGAGCCGGCCAGGGCTTCCACGCAGCCTTTCCC 121 Db 916 CCCTGCGATTCTCTGCTGCCAGAGCCGGCCAGGCGCTTCCACGGCAGCGCAGCCTTTCCC 975	Qy 122 CGGGCTGGGCTTGGAGTCGTCGTCGCTTCCCCAGTGCCCGCGGGTGAGCCTTCG 181 Db 976 C-GGCTGGGCTTGGAGTCGTTGGCTTCCCCAGTGCCCGCGGAGTGAGCCTTCG 1034	Qy 182 CCCCAGTCAGCCAAATGCTCCTCCTGGGCCTCCTGCTGACATCTGCCCTGGCCCTGGCCTGACATCTGCCCTGGCCTGCTGACATCTCCTCCTCCTGGCTGACATCTCCTCCTCCTGGCTGACATCTGCCCTGGCCGCGCTGGCCGGCC	Qy 242 AAAGAACGGGGACTCGGGCTGAGCTCAACCTGAGCAAGTTGCAGCTCTCCCGGCGACA 301 Db 1095 AAAGAACGGGGCTCGAGCTGAGCTCAACCTGAGCAGCAAGTTGCAGCTCTCCAGCCACA 1154	Qy 302 AGGAACAGAACGGAGTGCAAGATCCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG 361	Qy 362 GGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAAGAATATGGTGTGTGT
	1035 CCCCAGTCAGCCAAATGCTCCTCCTCGCCTCCTCCTGCTGACATCTGCCCTGGCCGGCC	2 AGGAACAGAACGGAGTGCAAGATCCCCGGCATGAGAGAGTTGTCACTATATCTGGTAATG	362 GGAGCATCCAGGAGTTTCCTCATACGTACCCAAGAATATGGTGCTGGTGTGGA 421	422 GATTAGTTGGAGTAGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481 1275 GATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334	482 TGGAAGATCCAGAAGATATATGCAAGTATGATTTTGTAGAAGTTGAGGACCCAGTG 541 	542 ATGGAAGTGTTTAGGACGCTGGTGGTTCTGGGACTGTGCCAGGAAAGCAGACTTCTA 601 1395 ATGGAAGTGTTTTAGGACGCTGGTGGTTCTGGGACTGTGCCAGGAAAGCAGACTCTA 1454	602 AAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGAT 661 	662 TCTGCATCCACTACAGTATTATCATGCCACAAGTCACAGAAACCACGAGTCCTTCGGTGT 721 	722 IGCCCCTICATCITIGICATIGGACCIGCICAACAAGGIGTGACTGCCTICAGIACCT 781	782 TGGAAGAGCTGATTCGGTACCTAGAGCCAGATGGAGGGGGGGG	842 ACAAGCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCCAAGAGGG 901 	902 IGAATCTGAATCTCCTCAAGGAAAGAGTAAAACTCTACAGCTGCACACCCCGGAACTTCT 961 	962 CAGTGTCCATACGGGAAGAGCTAAAGACGACACATACCATATTCTGGCCAGGTTGTCTCC 1021 	1022 TGGTCAAGCGCTGTGGAAGAAATTGTGCCTGTTGTCTCCATAATTGCAATGAATG	1082 GTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAAACTG 1141 	1142 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCACGAGGAATGTG 1201 	1202 ACTGTGTGTGTAGAGGAAACGCAGGAGGGTAACTGCAGCCTTCGTAGCAGCACACACGAGA 1261	1262 CACTGGCATTCTGTGTACCCCCAAGCAACCTTCATCCCCACCAGCGTTGGCCGCAGGG 1321
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                         Sequence 3, Application US/10264361

GENERAL INFORMATION:
APPLICANT Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
FILE REPERENCE: 00-53
CURRENT APPLICATION NUMBER: US/10/264,361
CURRENT FILING DATE: 2002-10-03
FR.OR APPLICATION NUMBER: US/09/695,121
FR.OR PELLOR PILING DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE FRABESEQ for Windows Version 3.0
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                          Score 1444.8;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.4%;
Matches 1460; Conservative
                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-10-264-361-3
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ORGANISM: Mus musculus
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RESULT 14
US-10-264-361-3
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                        TGCCCCTTGATCTTTGTCATTGGACCTGCTCAACAATGCTGTGACTGCCTTCAGTACCT
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                                                                            TGGAAGATCCAGAAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCCCAGTG
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     GATTAGTTGCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC
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search completed: November 26, 2003, 08:55:02
Job time : 3152.15 secs

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Sequence 58, Appl
Sequence 2384, Appl
Sequence 231, Appl
Sequence 137, Appl
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US-10-648-593-58

US-0-60-511-2084

US-0-485-450-131

US-09-816-133-12

US-09-876-813-12

US-09-876-813-12

US-09-457-066-50

US-09-457-066-50

US-09-457-066-50

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US-09-457-066-50

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US-09-876-813-6

US-09-876-813-6

US-10-321-962-7

US-10-606-055-3

US-10-606-055-3

US-09-876-813-6

US-10-606-055-3

US-09-876-813-6

US-10-606-055-3

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242 AAAGAACGGGGACTCGGGCTGAGTCCAACCTGAGCAGCAAGTTGCAGCTCTCCAGCGACA 301

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Oy 1382 TIGITIGCTTCAAIAGCCTTCCCCTGCAGACTTCAAGTGTCTTCTAAAAGACCAGAGGC 1441 Db 2235 TIGITIG	RESULT 2 US-09-876-813-34 ; Sequence 34, Application US/09876813 ; GENERAL INFORMATION: ; APPLICANT: Gilbert, Teresa ; APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Sheppard, Paul O.	TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4 FILE REFERENCE: 99-19 FURRENT APPLICATION NUMBER: US/09/876,813 CURRENT FILING DATE: 2001-06-06 FRIOR APPLICATION NUMBER: US/09/564,595 FRIOR FILING DATE: 2000-05-03 PRIOR APPLICATION NUMBER: US/09/564,595 PRIOR FILING DATE: 1999-05-03	FRIOR FILING DATE: 1999-11-10 PRIOR FILING DATE: 1999-11-10 PRIOR FILING DATE: 2000-02-04 PRIOR FILING DATE: 2000-02-04 NUMBER OF SEQ ID NOS: 57 SOFTWARE: FastSEQ for Windows Version 4.0	Mus musc CDS	JOCATION: (1049/)(2086) US-09-876-813-34 Usery Match 98.0%; Score 1444.8; DB 5; Length 3571;	Matches 1460; Conservative 0; Mismatches 8; Indels 1; Gaps 1; Qy 2 ACCTGGAGACGGGGCTCTAGGAAAATTTTGGATGGGATTATGTGGAAACTA 61		CCCTGCGATTCTCTGCTGCTGCCGGCCGGCCTTCCACCGCAGCGCAGCTTTCCC CGGGCTGGGGTTGAGCCTTGGAGTCGTCGTCGCTTCCCCAGTGCCCGCGAGTGAGCCCTTCG	Db 976 ċ-ĠĠĊŢĠĠĠĊŢŦĠĠĠĠŢĠĠŢŢĠĠĊŢŦĊĊCĊĠĠŢŢĠĊĠĠĠĠĠĠĠĠĠĠ	Db 1035 CCCAGTCAGCCAACTCCTCCGGCCTCCTCTGCTGCACATCTGCCCTGGCCGGCC	Db 1095 AAAGAACAGAGACTCGAGCTCAACTCCAACCAGCAAGTTGCAGCTCCCAGCGACA 1154 Ov 302 AGGAACAGAACAGAGTCCAAGATCCCCGCCATGAGAGAGTTGTACTATATCTGGTAATG 361	1155	QY 362 GGAGCATCCACAGAGTTTCCTCATACGTACCTAGAAAATATGGTGCTGGTGGA 421 nh 1915 GCAGGATCCACAGAGTTTCCTCATACATACCTAACCCAAAAAATATGGTGCTGGAATATGGTGCTGGTGGTGGTAGTGTGGTGGTGGTGGTGGTGGTGGTGGTG	422 GATTAGTIGCAGTAGATGAGAAATGTIGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC
QY 302 AGGAACAGAACGGAGTGCAAGATCCCCGGCATGAGAGATGTCACTATATCTGGTAATG 361 Db 1155 AGGAACAGAACGGAGTGCAAGATCCCCGCATGAGAGTTGTCACTATATCTGGTAAT 1214 QY 362 GGAACATCCACAAGATCCCCAAGAAATATGGTGTGTGTGT	Qy 422 GATTAGTIGCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 481 Db 1275 GATTAGTTGCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 1334 Qy 482 TGGAAGATCCAGAAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCCAGTG 541 Db 1335 TGGAAGATCCAGAAGACGATATATGCAAGTATGATTTTGTAGAAGTTGAGGAGCCCAGTG 1394	542 1395 602	662 TCTGCATCCACTACAGTATTATCATGCCACAAGTCACAGAAACCACGAGTCCTTCGGTGT	ccccttcat aagagctga aagagctga	OY 842 ACAAGCCAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAAGTGG 901	QY 902 TGAATCTGAATCTCCTCAAGGAAGAGTAAAACTCTACAGCTGCACACCCGGAACTTCT 961 Db 1755 TGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACAGCTGCACACCCCGGAACTTCT 1814	OY 962 CAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGTCTCC 1021 Db 1815 CAGTGTCCATACGGGAAGAGGTCAGAGACAGATACCATATTCTGGCCAGGTTGTCTC 1874	OY 1022 TGGTCAAGCGCTGTGGAGAAATTGTGCCTGTTGTCTCCATAATTGCAATGAATG	QY 1082 GTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAACTG 1141 Db 1935 GTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAAACTG 1194 Db 1935 GTGTCCCACGTAAAGTTACAAAAAGTACCATGAGGTCCTTCAGTTGAGACCAAAAACTG 1994	QY 1142 GAGTCAAGGGATTGCATAAGTCACTCACTCATGTGGCTCTGGAACACCCCGAGGAATGTG 1201 Db 1995 GAGTCAAGGGATTGCATAAGTCACTCACTGATGTGGCTCTGGAACACCACGAGGAATGTG 2054	Qy 1202 ACTGTGTGTGTGTGAGGAAACGCAGGAGGGTAACTGCAGCCTTCGTAGCAGCACACGTGAG 1261 Dh 2055 ACTGTGTGTGTAGAGGAAACGCAGAAGGTAACTGCAGCCTTCGTAGCAGCAAACGGAGCATAACTGCAGCACACACA	1262 CACTGGCATTCTGTGTACCCCCACAACCTTCATCCCCACCACGAGGGCGTTGGCCGCAGGG	2115	control

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                                                                             PROMOTING GROWTH OF
                                                                                                                                                                                                                                                                                                                                                                                                 8,
Sequence 3, Application US/10664432;
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROW:
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/10/664,432
CURRENT FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 3571
                                                                                                                                                                                                                                                                                                                                                             Score 1444.8;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 99.4%;
Matches 1460; Conservative
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; LOCATION: (1049)...(2086)
US-10-664-432-3
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Query Match 62.0%; Score 914.2; DB 1; Length 3007; Best Local Similarity 83.5%; Pred. No. 6.6e-285; Indels 4; Gaps 1; Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1; V 2 ACTGGAGACACAGAGGGCTCTAGGAAAATTTTGGATGGGATTATGTGGAAACTA 61 1 1	CTCGCCCCAGTCAGCCAAATGCTCCTCCTCCTCCTCCTCGCTGCTCCTGCCCTGGCC CTCGCCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGCTGACATCTGCCCTGGCC GCCCAAAGAACGGGAATGAGCCTCTTCGGGCTTCTCCTGCTGACATTGCCCTGGCC GGCCAAAGAACGGGGACTCGGGCTGAGCTGA	2 2 2 2 4 8 4 8 4 8 4 8 4 8 4 8 4 8 4 8	418 TGGAGATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGAGATTTGTGAGAGTTTTGTGAGAGTTTTTGTTGATGAGAGTTTTTT	774 538 834	598 TCTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCC 657	1014 ACTIGGAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG		898 GTGGTGAATCTCGTCAAGGAAAAGGTAAAACTCTACAGGTGCAAACCCGGAAC 9 [958 TTCTCAGTGTCCATACGGGAAGAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGT 1017	1018 CTCCTGGTCAAGCGCTGTGGAAAATTGTGCCTGTTGTCTCCATAATTGCAATGAATG
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Qy 538 AGTGATGGAAGACGATATATGCAAGTATGTATATTGTAGAAGTTGAGGAGCCC 537 Db 774 GGGCTTGAAGACCACAAGATGACATATGCAAGTATGTATTTTTGTAGAGTTGAGGAACCC 833 Qy 538 AGTGATGGAAGTGTTTTAGGACGCTGGTGTGGTTCTGGGACTGTGCCAGGAAGCAGCT 597 Db 834 AGTGATGGAAGTATTTTAGGACGCTGGTGTGGTTCTGGACTGTACCAGGAAACAGATT 893 Qy 598 TCTAAAGGAAATCATATAGGACGCTGGTGTGGTTCTGGTACTGTACTGTACTGAACCC 657 Db 894 TCTAAAGGAAATCAATAAGAATTATGTATCTGATGAATTTTCCTTCTGAACCC 657 Qy 658 GGATTCTGCATCAACTAATAACATATATCATGCACAAGAAACCAGAACCTTCGAACCA 953 Qy 658 GGATTCTGCATCAACTAATATCATGCACACAAGAACCAGAACCTTCGAACCA 953 CATTCTTGATCCAATAATAACATATATCATGCACACAAGAACCACAGACCCTTCG 177	118 GTGTTGCCCCTTCATCTTTGTCATTGGACCTGCTCAACAACGATCGTGACTGCCTTCAGT	0.00 0.00	RESULT 6 US-60-507-511-2084 Sequence 2084, Application US/60507511 Sequence 2084, Application US/60507511 Sequence 2084, Application US/60507511 TITLE OF INVENTION: UNCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITTING OF INVENTION: UNCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITTING OF INVENTION: HUMAN OSTECARTHRITIS AND HUMAN PROTEASES FILE REFERENCE: AM 101081 CURRENT APPLICATION NUMBER: US/60/507,511 CURRENT PAPLICATION NUMBER: US/60/507,511 CURRENT PAPLICATION OSS: 2003-10-02 NUMBER OF SEQ 1D NOS: 2036-33 SOFTWARE: PatentIn version 3.2 SEQ 1D NO 2084 LENGTH: 3007 TYPE: DNA ORGANISM: Homo sapiens US-60-507-511-2084 Query Match 62.0%; Score 914.2; DB 7; Length 3007;
	RESULT 5 US-10-648-593-58 US-10-648-593-58 Sequence 58, Application US/10648593 Sequence 58, Application US/10648593 Sequence 58, Application US/10648593 GENERAL INFORMATION: TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS FILE REFERENCE: D0273 NP CURRENT APPLICATION NUMBER: 06/406,385 PRIOR FILING DATE: 2003-08-27 NUMBER OF SEQ ID NOS: 557 SOFTWARE: Patentin version 3.2 SEQ ID NO S8 LENGTH: 3007 TYPE: DNA CRANICSH: DNA	Query Match 62.0%; Score 914.2; DB 6; Length 3007; Best Local Similarity 83.5%; Pred. No. 6.6e-285; Indels 4; Gaps 1; Matches 1050; Conservative 0; Mismatches 203; Indels 4; Gaps 1; Qy 2 ACTGGAGACACAGAAGAGGGCTCTAGGAAAATTTTGGATGGGATTATGTGGAACTA 61	0y 178 CTGGCCCCAGTCAGCCAAATGCTCCTCCTCCTCCTGCCTG

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                         <u> AGTGATGGAAGTGTTTTAGGACGCTGGTGTGGTTCTGGGACTGTGCCAGGAAAGCAGACT</u>
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APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND ITLE OF INVENTION: THERROF
FILE REFERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 137
LENGTH: 3007
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ORGANISM: Homo sapiens
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APPLICANT: Gao, Zerrles E.
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher
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APPLICANT: YUE, Henry
APPLICANT: YUE, Henry
APPLICANT: CORLEY, Neil C.
APPLICANT: CORLEY, Neil C.
APPLICANT: GUEGLER, Karl J.
APPLICANT: GUEGLER, Karl J.
APPLICANT: GUEGLER, Karl J.
APPLICANT: AU-YOUNG, Janice K.
TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES
FILE REFERENCE: PF-0627 USN
CURRENT APPLICATION NUMBER: US/09/830,320A
CURRENT APPLICATION NUMBER: US/09/830,320A
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
PRIOR PRILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
SEQ ID NO 8
TANGER OF SEQ ID NOS: 12
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; OTHER INFORMATION: Incyte ID No.: 4163378CB1
US-09-830-320A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 8, Application US/09830320A; GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; APPLICANT: TANG, Y. Tom
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ORGANISM: Homo sapiens
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APPLICANT: HARL, Charles E.
APPLICANT: HARL, Charles E.
APPLICANT: HARL, Charles E.
TILE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT FILING DATE: 2001-06-06
FRIOR PILING DATE: 2000-05-03
FRIOR PILING DATE: 1999-06-03
FRIOR FILING DATE: 1999-06-03
FRIOR FILING DATE: 1999-010-06-03
FRIOR FILING DATE: 1999-010-06-03
FRIOR FILING DATE: 2000-02-04
FRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SORTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 32
SEQ ID NO 35
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                                                                                 823 GTGGACTTGGACAGCCTCTACAAGCCAACATGGCAGCTT
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; LOCATION: (154)...(1191)
US-09-876-813-32
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ORGANISM: Homo sapiens
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US-09-876-813-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1760;
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APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3;
FILLE REPERBENCE: 98-60.
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FactSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 878.8; DB 5;
Pred. No. 1.5e-273;
0; Mismatches 197;
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Best Local Similarity 83.4%;
Matches 1011; Conservative
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US-09-457-066-1
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICANT: 2003-09-19
CURRENT APPLICANTON WINBER: US/10/664,432
CURRENT FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASISEQ for Windows Version 3.0
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                                                                                             1201 CACCAGCAGCTC 1212
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US-10-664-432-1
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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Matches 1011; Conserv
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                                                                             222
                                                                                                   CGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAATGAGCCTCTTCGGGCTTCTCCTGCTG 180
                                                                                                                                                                             ACATCTGCCCTGGCCGGCCAGAGACAGGGACTCAGGCGGAATCCAACCTGAGTAGTAAA 240
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                                                                                                                                                                                                                                                                                                         GICACIATATCTGGTAATGGGAGCATCCACAGCCCGAAGTTTCCTCATACGTACCCAAGA 402
                                                                                                                                                                                                                                                                                                                                                                               AATATGGTGCTGGTGTGGAGATTAGTTGCAGTAGAAAAATGTGCGGATCCAGCTGACA 462
                                                                                                                                                                                                                                                                                                                                                                                                                   AATACGGTCTTGGTATGGAGATTAGTAGCAGTAGGAAAATGTATGGATACAACTTACG 420
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                           CCGGCCAAAGAACGGGGACTCGGGCTGAGTCCAACCTGAGCAAGTTGCAGCTCTCCA
                                                    ccesccagadacaesesesesesesesesaarccaaecreaerasraaarrecaerrrreca
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                                  TTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAA
                                                              ACCACGAGICCTICGGIGITGCCCCCTICATCTITGTCATTGGACCIGCTCAACAATGCT
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Pred. No. 1.4e-230;
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US-09-457-066-50
Sequence 50, Application US/09457066
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Shempard, Paul O.
APPLICANT: Shempard, Paul O.
APPLICANT: Globenter, Kimberly E.
APPLICANT: Globenter, Kimberly E.
APPLICANT: Globenter, Kimberly E.
APPLICANT: Globenter, Kimberly E.
APPLICANT: Globenter, Kimberly E.
APPLICANT: West, James W.
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEC for Windows Version 3.0
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ORGANISM: Artificial Sequence
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US-09-457-066-50
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Best Local Similarity
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APPLICANT: TUTNER, C. Alexander Jr.
APPLICANT: Donoho, Gregory
APPLICANT: Hohls, Michael
APPLICANT: Hehls, Michael
APPLICANT: Ambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
TITLE OF INVENTION: Novel Human Proteins
FILE REFERENCE: LEX-0070-PCT
CURRENT PAPLICATION NUMBER: PCT/US00/28803
CURRENT FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO 6
LENGTH: 918
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35.2%; Score 519; DB 1; Length 91
Best Local Similarity 83.1%; Pred. No. 4.2e-157;
Matches 591; Conservative 0; Mismatches 120; Indels
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Sequence 6, Application US/09457066
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Alarty Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
FILLE REFERENCE: 98-60
CURRENT FILLS NETERENCE: 98-60
CURRENT FILLS (PAUL OF DATE: 1999-12-07)
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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) LOCATION: (1)...(1035)

; OTHER INFORMATION: n = A,T,C or G

US-09-457-066-6
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ORGANISM: Artificial Sequence
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Search completed: November 26, 2003, 09:11:10 Job time : 275.739 secs

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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Minimum Maximum

Database

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Itoh, M., Komno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
11042159
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Mus musculus 15 days embryo head cDMA, RIKEN full-length enriched library, clone:D930001M08 product:platelet-derived growth factor, c polygeptide, full insert sequence.

AK052947.1 G1:26343118

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (hordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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BQ957838
BQ968266
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AUTHORS
TITLE
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BCO29099 Mus muscu
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l to the score of the result being printed,
of the total score distribution.
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                    GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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1444.8 1444.8 1444.8 1366.2

Score

Result No.

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/tissue_type="head"
/clone lib="RIKEN full-length enriched mouse cDNA library"
/dev stage="15 days embryo"
                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD|MGI:1859631, GB|NM_019971, evidence: BLASTN, 99%, match=2691)
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                                                                                                                          /db_xref="FANTOM_DB:D930001M08"
/db_xref="taxon:10090"
/clone="D930001M08"
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                                              organism="Mus musculus"
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                                                                     'mol type="mRNA"
'strain="C57BL/6J"
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RHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDD
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                                                                                   Physical and Chemical Research (RIXEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIXEN Yokohama Institute; 1-7-22 Subeliro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.go.jp, PRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Enx:81-45-503-9216
Enx:91-45-503-9216
Encyclopedia Project of Genome Exploration Research Genome Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        736
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             Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
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Please visit our web site for further details.
URL:http://ganome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="F8NTOM DB:9130403008"
/db_xref="taxon:10090"
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/sex="male"
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Adachi, J., Azawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Pukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hiramoto, K., Hiraoka, T., Hirozane, T., Hayashida, K., Hayatsu, M., Hiramoto, K., Hiraoka, T., Harozane, T., Hari, Kawai, J., Kojima, Y., Kondo, S., Komo, H., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komo, H., Koda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, K., Sakazume, N., Sagabe, Y., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yasunishi, A., Direct Submission

L. Submitted (16-Jul-201) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan (E-mail:genome-reseascrike...gen, 145-503-9222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222, 145-8222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
                                                                                          Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3405)
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                                                               The FANTOM Consortium and the RIKEN Genome Exploration Research
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/mol type="mRNR"
/strain="CSTBL/61"
/db_xref="FaNTOM DB:A730022G11"
/db_xref="taxon:I0090"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730022G11 product:Platelet-derived growth factor, C polypeptide, full insert sequence.
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                                   TIGITIGCTICAATAGCCTTCCCCTGCAGACTTCAAGTGTCTTCTAAAAGACCAGAGGC 1441
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
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Clone distribution: MGC clone distribution information can be fount through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 35 Row: p Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10242384
This clone has the following problem: frame shifted.
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Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2893)
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Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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/clone="IRMAGE:366079"
/tissue_type="Wammary tumor metastatized to lung:
MMTV-LITR/Watcl model. Expression driven by an MMTV-LIR
                                                                                       ACTGTGTGTGTAGAGGAAACGCAGGAGGTAACTGCAGCCTTCGTAGCAGCACACGTGAG
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Mus musculus, Similar to platelet derived growth factor, polypeptide, clone IMAGE:3660797, mRNA.
BC029099.1 GI:20809397
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/organism="Mus musculus"
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/strain="CZECH II"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 902)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14092 row: j column: 01
High quality sequence stop: 735.
High quality sequence stop: 735.
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/clone_lib="NCI_CGAP_Lu30"
/lab_höst="DH10B"
/note="Vector: pCMV-SPORT6"
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Pred. No. 0;
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Best Local Similarity 95.2%;
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Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:Cl30008P20 product:platelet-derived growth factor, C polypeptide, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                    780 CAGCCTCTACAAG-CAACATGGCAGCTTTTGGGCAAGGCTTTCCTGTATGGAAAAAAA
                                           CAAAGTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACAGCTGCACCCCG
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Nature 409 (6821), 685-690 (2001)
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//cloud lib="NCI_CGAP Mam2"
//note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Homo sapiens, Similar to platelet-derived growth factor, C
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2826)
Strausberg, R.
Direct Submission
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                                                                    AGCATCCACAGCCCGAAGTTTCCTCATACATACCCAAGAAATATGGTGTGTGGAGA
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                                                                      The FANTOW CORDSTILUM and the KIKEN Genome Exploration Kesearch Group phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs

B (Bases 1 to 2502)

Adachi, ., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanadaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayasua, T., Kondo, S., Konno, H., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kaya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Askazume, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sakai, K., Sahazume, N., Sano, H., Sakai, K., Sakazume, N., Sano, H., Sakai, K., Sakazume, N., Sano, H., Sakai, K., Sakazume, N., Sano, H., Shizaki, T., Sanamatau, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Arkeda, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Muramatau, M., and Hayashizaki, Y. Direct Submission Hayashizaki, Y. Direct Submission and Chemical Research (RIKEN) (Boomeic Sciences Center (GSC), RAKIEN Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama Institute, 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama Lastine, Japan (E-mail:genome-res@gsc.riken.go.jp/, Tel:81-45-503-9222, CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Physical Physical Animal Research in Riken contributed to brepare mouse tissues.
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/dev_stage="16 days embryo"
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/note="platelet-derived growth factor, C polypeptide
(MGD|MGI:1859631, GB|NM_019971, evidence: BLASTN, 998,
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
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Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Musmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musmalia, Eutheria, Po 823)
I (bases 1 to 823)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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UI-M-EVO-cbh-b-02-0-UI.rl NIH EMAP_EVO Mus musculus cDNA clone
UI-M-EVO-cbh-b-02-0-UI 5', mRNA sequence.
BU614825
BU614825.1 GI:23281040
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TGGGCTGGAAGATCCAGAAGACGATATATGCAAGTATGATTTTTGTAGAAGTTGAGGAGCC
                        537 CAGTGATGGAAGTGTTTTAGGACGCTGGTGTGTGGTTCTGGGACTGTGCCCAGGAAAGCAGAC
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Location/Qualifiers
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                                                                                                                                                               Web site: http://www-shgc.stanford.edu contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
  USA

MIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLOMTROH

CDNA Library Preparation: CLOMTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

CDNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, WWW-shgc.stanford.edu
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/organism="Homo sapiens"
/do xref="texon:9606"
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/fissue Fype="Kidney"
/clone Iibb="NIH MGC 75"
/lab_host="DH10E"
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Best Local Similarity 79.5%;
Matches 1048; Conservative
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausherg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausher, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Butcow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Godin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosk, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
Human, A.M., Schein, J.E., Jones, S.J. and Marza, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC051876 2655 bp mRNA linear HTC 05-MAY-2003
Homo sapiens cDNA clone IMAGE:6527736, containing frame-shift
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2655)
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Direct Submission
Submitted (01-MAY-2003) National Institutes of Health, Mammalian
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  TIGCAATGAATGTCAGTGTCCCCACGTAAAGTTACAAAAAAGGTACCATGAGGTCCTTCA
                                                                                                                                                                                                   1185 ACACCACGAGGAATGTGACTGTGTGTGTAGAGGAAACGCAGGAGGGTAACTGCAGCCTTC
                                                                                        601 ACACCACGAGGAATGTGACTGTGTGTAGAGGAAACGCAGGAGGGTAACTGCAGCCTTC
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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/dev stage="whole brain"
/dev stage="whole brain"
/lab_host="holio brain"
/lab_host="holio brain; brain; Vector: pYX-Asc; Site_1: EcoR I;
/clone lib="WINH BMAP EVO"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according to Sonable, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNa was size fractionated on a 1% agarose gel: First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Henin Chin, Ph.D., program coordinator:"
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
Seq primer: pyx.5.
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Pred. No. 4.3e-216;
0; Mismatches 3;
                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6"
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Best Local Similarity 99.5%;
Matches 820; Conservative
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PUYS/838 901 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8860959 NCI CGAP Mam2 Mus musculus cDNA clone
IMAGE:6440547 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                 GAGCTAAAGAGGACAGATACCATATTCTGGCCAGGTTGTCTCCTGGTCAAGCGCGCTGTGGA
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                                                                                                                    TATCTTGAACCAGAGAGAGATGGCAGTTGGACTTTAGAAGATCTATATAGGCCAACTTGGCAA
                                                                                                                                                         CTTTTGGGCAAGGCTTTCCTGTATGGGAAAAAAGCAAAGTGGTGAATCTGAATCTCCTC
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                                                   ccacriggaccrigariaaraarigcraraacrigccrirragraccrirggaagaccrrarricga
                                                                                      TACCTAGAGCCAGATCGATGGCAGGTGGACTTGGACAGCCTCTACAAGCCAACATGGCAG
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Producement: Gilbert Smith, Ph.D.

Tissue Producement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information and through the I.M.A.G.E. Consortium/LIML at:

http://image.llnl.gov f column: 04

High quality sequence stop: 669.
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/clone="IMAGE:6440547"
/tissue_type="tumor, biopsy sample"
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/strain="FVB/N-3"
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Meb site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGCTGGAAGATCCAGAAGAC 498
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                                                                                                                      Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 110 Row: p.Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggagrogerecriceaaagroceeeeereagrogeereageerereaeeeeagreageeaaarga 75
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                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE":5527736"
/tissue=type="Uterus, leiomyosarcoma"
/clone_lib="NIH MGC_71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 757.6; DB 11;
Pred. No. 2.6e-201;
0; Mismatches 179;
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/crouse_laber_win_wac_lal.
//crouse_laber_win_wac_lal.
//crouse_laber_win_wac_lal.
Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 tetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TGTGTCTACTACTAGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                readdaacccagrgardaacrararraaddcccccccrccrccrccrccrccrccacc 360
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    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LINL at:
http://image.llh.gov
Plate: LiAM12833 row: k column: 23
High quality sequence stop: 676.
               Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
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Pred. No. 7.8e-162
                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5770510"
/lab_host="DH108"
/clone_lib="NIH_MGC_121"
                                                                                                                               Contact: Robert Strausberg, Ph.D.
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Matches 738; Conservative
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AUTHORS
TITLE
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/dev_stage="5 months"
/lab_host="DH108"
/clone_lib="NGI_CGAP_Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
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Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
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                                                                                                                                                                                                              Score 707; DB 13;
Pred. No. 2.3e-187;
0; Mismatches 2;
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Mus musculus
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Musmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 877)
NIH-MGC http://mgc.nci.nih.gov/.
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                                           Length
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                                        Score 597.6; DB 10;
Pred. No. 1.4e-156;
0; Mismatches 25;
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/note="Organ: mammary; Vector: pCMV-SPORTS; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
220 c 250 g 198 t
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NIH-MGC http://mgc.nci.nih.gov/.
Nati-MGC http://mgc.nci.nih.gov/.
Ontublished
Contact: Robert Strausberg, Ph.D.
                                                   GAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAAC
                                                                                                                                                 AAAAAGCAAAGTGGTGAATCTGGAATCTCCTCAAGGAAGAGGTAAAACTCTACAGCTGCAC
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Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Tncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can bfound through the I.M.A.G.E. Consortium/Link at:
http://image.llh.gov
Plate: LiAM10323 row: d column: 19
High quality sequence stop: 690.
Location/Qualifiers
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/clone="INAGE:443938"
/tiseue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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Mus musculus
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712 bp mRNA linear EST 18-SEP-2001 63343666F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5371337 5', B1693338
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/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Glibert Smith, NIH"

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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 712)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. column: 18
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                                              913 CTCCTCAAGGAAG--AGGTAAAACTCTACAGCTGCACACCCCGGAACTTCTCAGTGTCCA
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National Institutes of Health, Mammalian Gene Collection
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/mol_type="mRNA"
/strafn="FVDN-1"
/db xref="taxon:10090"
/clone="IMAGE:5371337"
/tissue_type="tumor, biopsy sample"
/dev.stage="5 months"
/lab_host="DH108"
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Location/Qualifiers
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Matches 606; Conserv
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                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.lln.gov

Plate: LLAMBQ243 row: o column: 08

High quality sequence stop: 677.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="NCI CGAP Lu30"
//oloe="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sal1; transgenic model WNT-1, expression driven by
MMY-LIR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCCGGATTCTGCATCCACT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTGTCATTGGACCTGCTCAACAATGCTGTGACTGCCTTCAGTACCTTGG-AAGAGCTG 792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 AAGACGATCTATGCAAGTATGATTTTGTAGAAGTTTGAGGAGCCCAGTGATGGAAGTGTT 269
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                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:4008799"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 595.6; DB 10; Length
Pred. No. 5.2e-156;
0; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 677)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Muramatsu, M., and Hayashizaki, Y., Tanaka, T., Toya, T., Toya, T., Tanamatsu, M., and Hayashizaki, Y., Tanaka, T., Toya, T., Toya, T., Tanamatsu, M., and Hayashizaki, Y.,
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URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,M., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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The Institute of Physical and Chemical Research (RIXEN)
1-7-22 Subtitute of Physical and Chemical Research (RIXEN)
1-7-22 Subtitute of Physical and Chemical Research (RIXEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
AAAGAGGACAGATACCATATTCTGGCCAGGTTGTCTCCTGGTCAAGGGCTGTGAGAAA 180
                                                                                                                                                                                                                                                                                                481 ATGGTAAAGATCTTACTCGTCTCCAACCAAATTCTCAGTTGTTTGCTTCAATAGCCTTCC 540
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JOURNAL
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FIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Pukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                       Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 15 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
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/lab_host="DH10B"
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317 AAAGAACGGGGACTCGGGCTGAGTCCAACCTGAGCAGCAAGTTGCAGCTCTCCAGCGACA 376

GATTAGTTGCAGTAGATGAAAATGTGCGGATCCAGCTGACATTTGATGAGAGTTTGGGC 481 497 GATTAGTTGCAGTAGATAAATGTGCGGATCCAGCTGACATTTGATGAGAGATTTGGGC 556

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AAY41766 AAY30023 AAB48657 AAB24250 AAB4322 AAB10633	AAB10644 AAB10650 AAB10651 AAB19578 AAB3414 AAB24412 AAB01419 AAY59285	AAGSS603 AAU08465 AAU12314 AAB14028 AAB02649 AAB00997 AAB49895 AAB79894	ABS69269 ABB81331 AAB47689 AAU76684 ABU66712 ABU6698 ABU59793 ABU61152 ABG72132
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ALIGNMENTS

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Mouse; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; murine; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia;
                        AAB48658 standard; Protein; 345 AA
                                                                                                                                                                                                                                                                                                       03-MAY-2000; 2000WO-US40047.
                                                                                                                                                                                                                                                                                                                                  99US-0304216.
                                                                                                                                                                                                                                                                                                                                             10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
                                                                                                      Mouse zvegf3, SEQ ID NO:35.
                                                                             (first entry)
                                                                                                                                                                                                 immunomodulation; hepatic
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                                                                                                                                                                                                                         Mus musculus
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10-NOV-1999;
                                                                           09-MAR-2001
                                                                                                                                                                                                                                                                              09-NOV-2000
                                                    AAB48658;
RESULT 1
            AAB48658
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Gilbertson DG;

Hart CE, Sheppard PO,

Gilbert T,

26-SEP-2000 (first entry)

AAY96861;

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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

CC (AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

CC characterised by a PDGF cystine knot structure, and a CUB domain

Growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

CC characterised by a PDGF cystine knot structure, and a CUB domain

CC (AAB48655) which has a bera barrel structure. Zvegf4 has PDGF-like

activity, having mitogenic activity on fibroblasts, vascular smooth

cuscic cells and pericytes, and has also been shown to stimulate bone

activity, having mitogenic activity on fibroblasts, vascular smooth

cuscic cells and pericytes, and has also been shown to stimulate bone

CC growth. The invention also relates to fusion proteins comprising human zvegf4

cucleic acids; the recombinant expression of human zvegf4, an antibody

which binds to human zvegf4 or a fragment famina zvegf4, an antibody

which binds to human zvegf4 or a fragment activin, migration or

method of modulating the proliferation, differentiation, migration or

coll-surface PDGF receptor using a zvegf4-derived polypeptide; a

coll-surface PDGF receptor using a zvegf4-derived polypeptide;

a cell-surface PDGF receptor using a zvegf4-derived polypeptide;

complements may be used to stimulate tissue development or repair, or

creament or repair of liver damage, and mey also be used to

collular differentiation or proliferation. They are particularly used

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                                                                                                  Growth factor homologs and the nucleic acids that encode them, useful e.g. for treating liver damage, ischemia, multiple sclerosis and
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                                                                                                                                                                                                                   Disclosure; Page 130-131; 143pp; English
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Best Local Similarity 100.
Matches 345; Conservative
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                       WPI; 2000-687541/67.
N-PSDB; AAC81583.
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This shows a murine ZVBGF3 a novel vascular endothelial growth factor homologue. Polypeptides comprising an epitope-bearing portion human or murine ZVBGF3 are claimed. The growth factors comprises a growth factor domain and a CUB domain (generic sequence motifs are shown in AAY96859 and AAY96860). The growth factor domain is characterized by an exrangement of cysteine residues and beta-strands that is characteristic of the "cysteine knot" structure of the platelet-derived growth factor (PDGF) family. The CUB domain shows homology to CUB domains in currentlins, human bone morphogenetic protein. To protein seminal plasma croptocin. Structural and Abmology predict that cortein, bovine acidic seminal fluid protein and Xenopus laevis tolloid-like protein. Structural analysis and homology predict that croptocins. The human zvegf3 gene has been mapped to chromosome 4q28.3. CyrGF3 polypeptides complex with a second polypeptide to form multimeric proteins. The human zvegf3 gene has been mapped to chromosome 4q28.3. CyrGF3 is useful for stimulating cell surface PDGF-alpha receptor and for inhibiting PDGF-alpha receptor mediated cellular processes. ZVEGF3 is useful for regulating (post-development) organ growth, regeneration and mindenance, as well as tissue maintenance and repair processes. ZVEGF3 antagonists are useful for treating cancer, rheumatoid arthritis, disbetic retinopathy, ischemia, vascular intimal hyperplasia, atherosclerosis, wound healing, chronic liver disease and haemangioma cformation. ZVEGF3 can also be used to modulate neurite growth and for development of the nervous system, and for treating neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel zvegf3 polypeptides and nucleotides encoding them useful for
stimulating growth of smooth muscle cells and fibroblasts comprising an
epitope bearing portion of a specific amino acid sequence
                                                                                                                             Vascular endothelial growth factor; homologue; zvegf3; CUB domain; Cysteine knot; platelet-derived growth factor; PDGF; neuropilin; chromosome 4q28.3; cytostatic; anti-psoriatic; anti-inflammatory; anti-diabetic; ophthalmological; anti-rheumatic; anti-arthritic;
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                                                                                           Murine vascular endothelial growth factor homologue, ZVEGF3.
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99US-0161653.
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AAY96861 standard; Protein; 345 AA.

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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VBGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling.
Untela M, Alitalo K;
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Betsholz C;
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and/or growth or motility of cells expressing a PDGF-C receptor.

PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C. PDGF-C can also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation. PDGF-C antagonists can be used to inhibit tumour growth of a tumour expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choriocarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma and erythroleukemia, can be identified by testing for expression of PDGF-C pDGF-C antagonists can also be used to inhibit tissue

Common and the control of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions, especially found in the lung, kidney or liver.
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Matches 345; Conservative
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The patent discloses materials and methods for reducing cell
proliferation or extracellular matrix production, treating fibrosis and
ceducing stellate cell activation in a mammal. The method comprises
administering a composition containing a Evegf3 antagonist in combination
with a delivery vehicle. The Evegf3 is a protein that is structurally
related to platelet-derived growth factor (PDGF) and the vascular
endothelial growth factors (VEGF). The Evegf3 protein is also designated
cendothelial growth factors (VEGF). The Zvegf3 protein is also designated
an "VEGF-R" and "PDGF-C". The Zvegf3 antagonist is useful to block the
mitogenic effects of zvegf3 and thereby to inhibit or prevent and treat
keloids, scleroderma, fibrotic disorders of liver such as chronic active
hepatitis, fulminant viral hepatitis, post necrotic cirrhosis and
alpha-1-antitrypsin deficiency, fibrotic disorders of the kidney such as
diabetic glomerulosclerosis, focal glomerulosclerosis, diabetic
nephropathy, amyloidosis and renal arteriosclerosis, fibrotic disorders
of the lung such as silicosis, asbestosis, idiopathic pulmonary fibrosis,
bronchiolitis obliterans-organising pneumonia and pulmonary fibrosis,
tibrotic disorders of pancreas, fibroproliferative disorders of the
vasculature such as transplant vasculopathy and fibroproliferative
disorders of the bone such as osteopetrosis and hyperostosis.
The present sequence is mouse Evegf3 protein.
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Mismatches 0; Indels
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100.0%; Pred. No. 4e
iive 0; Mismatches
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                                                                                                                                    12-NOV-1999; 99US-0165255
01-AUG-2000; 2000US-0222223
                                                                                 23-OCT-2000; 2000WO-US29270
                                                                                                                     99US-0161653
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Best Local Similarity 100.
Matches 345; Conservative
                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                   WPI; 2001-300278/31.
N-PSDB; AAD04650.
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WO200128586-A1
                                                                                                                                                                                                                                             Gilbertson DG;
                                                                                                                         21-OCT-1999;
                                        26-APR-2001
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The invention relates to an isolated polypeptide, designated zvegf3 reactuar endothelial growth factor-like protein) of 111-136 amino acid residues in length and comprises the sequence appearing as ABG92889 from amino acid residues 23-345. Also included are an isolated protein comprising a first polypeptide disulphide bonded to a second polypeptide, where each of the first and second polypeptides is from zvegf 3, and where the protein modulates cell proliferation, differentiation, metabolism or migration, the zvegf 3 encoding polynucleotides and zvegf 3 expression vectors and host cells. Zvegf 3 is useful as additives in tissue adhesives for promoting revascularisation of the healing tissue, for designing molecules that cardicovascular development, cartilage and limb development, and T and B-cell function, and for imaging tumours or other sites of abnormal cell
                                                                                                                                                    VEGF; vascular endothelial growth factor; zvegf 3; mouse; chromosome 3; cell proliferation; differentiation; metabolism; migration; revascularisation; solid tumour; diabetor retinopathy; psoriamis; revascularisation; solid tumour; diabetor retinopathy; inflammation; myocardial ischaemia; scleroderma; fibrosis; glomerulosclerosis; atherosclerosis; skin wound; ulcer; burn; skin grafting; female reproductive tract disorder; chronic liver disease; chrolid disorder; heart failure; neurodegenerative disease; multiple sclerosis; Parkinson's disease; Alzheimer's disease; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation and in gene therapy applications. The proteins are useful therapeutically to stimulate tissue development or repair, or cellular differentiation or proliferation, for stimulating the growth of fibroblast or smooth muscle calminating the growth of reagents in assays for determining circulatory level of the protein or standards in the analysis of cell phenotype, for identifying inhibitors of their activity which are useful for reducing the growth of solid tumours, for treating diabetic retinopathy, psoriasis, rheumatoid arthritis, various forms of cancers, autoimmune disease, inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polypeptide, designated zvegf3 useful for treating skin wounds, ulcers, burns, skin grafting, female reproductive tract disorders, Parkinson's disease, and Alzheimer's disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Piddington CS, Sheppard PO, Shoemaker KE;
ABG92894 standard; Protein; 345 AA.
                                                                                                                        Mouse VEGF-like protein zvegf 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 2; 68pp; English.
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99US-161653P.
99US-165255P.
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                                                                               (first entry)
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N-PSDB; ABS68648.
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                                                                                                                                                                                                                                                                                                                                                    neurite outgrowth
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12-NOV-1999;
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                                                                               19-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-2002
                                        ABG92894;
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(HART/)
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                                                                                                                                                                                                                                                                                                                                                                                                              LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
       formation, keloids, liver fibrosis, lung fibrosis (e.g. silicosis, asbestosis), kidney fibrosis (including diabetic nephropathy), glomerulosclerosis atherosclerosis, skin wounds, ulcers, burns, skin grafting, and female reproductive tract disorders, chronic liver disease (hepatitis), cirrhosis, Reye's syndrome, Wilson's disease, circulatory disorders e.g. heart failure, hepatic or portal vein thrombosis, cardiac selerosis, neurodegenerative diseases such as multiple sclerosis, parkinson's disease, Alzheimer's disease, and for regenerating neurite outgrowths following strokes. The gene for mouse zvegfi is located on chromosome 3. The present sequence represents zvegf 3.
                                                                                                                                                                                                                                        9
myocardial ischaemia, scleroderma, and reducing fibrosis, including scar
                                                                                                                                                                                                                  1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                                                                                                                                                                        MILLGLILLTSALAGORTGTRAESNISSKIQLSSDKEQNGVQDPRHERVVTISGNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; zvegf3; zvegf4; platelet derived growth factor; PDGF; homolog; growth; bone; ligament; cartilage; proliferation; osteoblast; chondrocyte; bony defect; fracture; bone graft; implant; periodontal pocket; osteoclast; bone marrow stem cell; osteoporosis.
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                                                                                                                                                                   DB 23; Length 345;
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                                                                                                                                                                                          0; Indels
                                                                                                                                                                  100.0%; Score 1848; DB 2:
100.0%; Pred. No. 4e-182;
tive 0; Mismatches 0
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99US-142576P.
99US-161653P.
99US-16525P.
2000US-193723P.
99US-0457066.
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Matches 345; Conservative
                                                                                                                                            345 AA;
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21-OCT-1999;
12-NOV-1999;
31-MAR-2000;
07-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse zvegf3
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                                                                                                                                            Sequence
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The sequences given in AAB47889-90 represent human and mouse zvegf3,
respectively. zvegf3 is a platelet derived growth factor (PDGF) homolog
and it was used in the method of the invention for promoting growth of
bone, ligament or cartilage and stimulating proliferation of osteoblasts
or chondrocytes in a mammal. The proteins used were preferably a dimeric
cor chondrocytes in a mammal. The proteins used were preferably a dimeric
cor protein, with a delivery vehicle. The method of th invention is useful
for promoting growth of bone, ligament or cartilage in a mammal, where
the composition is administered at a site of a bony defect, preferably
a fracture, bone graft site, implant site, or periodontal pocket, and
for stimulating proliferation of osteoblasts or chondrocytes in a
mammal. It is further useful for promoting proliferation of osteoblasts,
osteoclasts, chondrocytes or bone marrow stem cells, where the bone
marrow stem cells are harvested from a patient prior to culture. The
method is therefore useful for treating osteoporosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEVEBSDGSVL 120
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                                                                                                                                                                                                                                                                                       Promoting growth of bone, ligament or cartilage in a mammal, involves administering to the mammal a protein which comprises growth factor domain of zvegf3 protein, a homolog of platelet-derived growth factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 19-20; 31pp; English.
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                                                                                                            Gilbertson DG;
HART C E.
GILBERTSON D G.
                                                                                                                                                                                      2002-171026/22
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                                                                                                                                                                                                                            N-PSDB; AAI72444
                                                                                                            Hart CE,
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                                                                                                                                                                                                                                                                                                                                                  A transgenic animal over-expressing platelet derived growth factor C is useful to study and find therapy for disease associated with PDGF-C over-expression, including cardiac hypertrophy and fibrosis
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Mouse; transgenic animal; platelet derived growth factor C; PDGF-C; cardiac hypertrophy; fibrosis.
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Best Local Similarity 100.
Matches 345; Conservative
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ABG76398 standard; Protein; 345 AA ABG76398; ABG76398
ID ABG
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AC ABG

22-MAY-2003 (first entry)

Mouse growth factor homologue, zvegf3.

portal vein thrombosis, cardiar sclerosis, new vessel formation; portal vein thrombosis, cardiar sclerosis, new vessel formation; organ transplant; tissue grafting; peripheral neuropathy; spinal cord; sensory neurite outgrowth; brain damage; head injury; paralysis; spinal injury; neurodegenerative disease; diabetic retinopathy; spinal cord; spinal injury; neurodegenerative disease; diabetic retinopathy; prostais; athoristis; scleroderma; keloid; liver fibrosis; psoriasis; proliferative vascular disorder; ocular neovascularisation; inflammatory disorder; rheumatoid arthritis; vascularisation; angiogenesis; nervous system disorder; cytostatic; hepatotropic; vulnerary; tranquilliser; cerebroprotective; neuroprotective; nootropic; ophthalmological; dermatological; coagulant; cardiant. Mouse; growth factor homologue; zvegf3; fibroblast; smooth muscle cell; cell-surface platelet-derived growth factor alpha receptor; PDGF; full-thickness skin wound; female reproductive tract; duodenal ulcer; prolonged bleeding; periodontal disease; tissue adhesive; liver damage; revascularisation; healing tissue; liver disease; CPC; CHN; cirrhosis; chronic active hepatitis; hepatic chronic passive congestion; stroke; central haemornhagic necrosis; hepatic vein thrombosis; ischaemia;

US2002177193-A1.

28-NOV-2002

2002US-0139583. 02-MAY-2002;

07-DEC-1998; 06-JUL-1999;

98US-111173P. 99US-142576P. 99US-161653P. 99US-165255P. 99US-0457066 07-DEC-1999; 21-OCT-1999; 12-NOV-1999

(ZYMO) ZYMOGENETICS INC.

Piddington CS, Sheppard PO, Shoemaker KE; CE, FILL Gilbertson DG, Hart

WPI; 2003-328485/31. N-PSDB; ABX93182.

New isolated zvegf3 polypeptide, useful for treating cancer, Alzheimer's disease, Parkinson's disease, chronic active hepatitis, hepatic vein thrombosis, comprises growth factor domain and CUB domain

Claim 1; Fig 6; 73pp; English.

The present invention relates to the isolation of a growth factor homologue referred to as zvegf3, and the polymucleotide sequence encoding It. The zvegf3 polypeptide is useful for stimulating the growth of fibroblasts or smooth muscle cells, or for activating a cell-surface platelet-derived growth factor (PDGF) alpha receptor. The zvegf3 polypeptide is useful as a PDGF alpha receptor agonist and thus is useful for treating full-thickness skin wounds, female reproductive tract and prolonged bleeding, periodottal disease, damaged liver tissue, and duodenal ulcers. The polypeptide is also useful as an additive in tissue adhesives for promoting revascularisation of healing tissue. The zvegf3 polypeptide is also useful for treating liver damage including damage due to liver disease, chronic active hepatitis, hepatic chronic passive congestion (CPC), central haemorrhagic necrosis (CHV), hepatic vein thrombosis, portal vein thrombosis, cardiac sclerosis, and many types of cirrhosis. The polypeptide is useful for enhancing expansion and mobilisation of endothelial precursor stem cells, creating and stabilising new vessel formation in areas requiring neovascularisation, including areas of ischaemia, organ transplants, wound healing, and tissue graffing. It may be used for treating peripheral neuropathies by increasing spinal

(GETH) GENENTECH INC.

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            treatment for the regeneration of neurite outgrowths following strokes, brain damage caused by head injuries, and paralysis caused by spinal hiluries. Application may also be made in treating neurodegenerative diseases (e.g. multiple sclerosis, Alzheimer's disease, Parkinson's disease), diabetic retinopathy, psoriasis, arthritis, scleroderma, and reducing fibrosis, keloids, liver fibrosis, lung fibrosis, khoney fibrosis, and glomerulosclerosis. An antibody that binds zvegf3 is useful for blocking the mitogenic, chemotactic, or angiogenic effects of zvegf3, and for treating proliferative vascular disorders, ocular neovascularisation, inflammatory disorders, rheumatoid arthritis, psoriasis, cancer, impaired or excessive vasculogenesis or angiogenesis, and diseases of the nervous system. The present sequence represents
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and sensory neurite outgrowth, and as part of therapeutic
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02-NOV-1998;
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tranquillizer, vulnery and cardiant activity. VBGF-E can be administered tranquillizer, vulnery and cardiant activity. VBGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially by expressing encoding polynucleotides, to regeneration, and may especially be used to treat cardiac hypertrophy. It can be combined with a carrier in pharmaceutical compositions, which can be administered to treat arrains thypertrophy. It can be combined with a carrier in pharmaceutical compositions, which can be administered to treat antiagonists and agonists, and the antagonists and administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose are also cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polymucleotides encoding the united of diagnose cardiovascular and endothelial disorders in the cancer of the cancer of the complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to diagnose a disease or susceptibility to a disease related to a mutated form of VEGF-E (e.g. a cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mutation in the VEGF-E-encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence represents the human VEGF-E protein described in the method of the invention.
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                                                                                                                                                             New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy
                                                                                                                                                                                                                                                                                 invention describes the isolation of a novel human vascular
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87.0%; Pred. No. 2.1e-163;
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Matches 300; Conservative
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                                             Ferrara N,
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RESULT 10

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29-APR-1998;
20-APR-1998;
30-APR-1998;
05-MAY-1998;
06-MAY-1998;
07-MAY-1998;
07-MAY-1998;
07-MAY-1998;
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07-MAY-1998;
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18-MAY-1998;
22-MAY-1998;
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                                                                                                          Human, PRO; EST; expressed sequence tag; PCR primer, hybridisation, probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
  Ā
AAY41766 standard; Protein; 345
                                                                                  Human PRO200 protein sequence
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98US-0080333.
98US-0080334.
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98US-0081952.
98US-0081955.
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98US-0082704
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98US-008336
98US-008332
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98US-00835499
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98US - 0077641.
98US - 0077649.
98US - 0078004.
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98US-0081817.
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98US-0082569.
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                                                        (first entry)
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15-APR-1998;
21-APR-1998;
21-APR-1998;
22-APR-1998;
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29-APR-1998;
29-APR-1998;
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12-MAR-1998;
13-MAR-1998;
17-MAR-1998;
20-1/AR-1998;
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20-WAR-1998;
20-WAR-1998;
25-WAR-1998;
26-MAR-1998;
27-WAR-1998;
27-WAR-1998;
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31-MAR-1998;
01-APR-1998;
01-APR-1998;
01-APR-1998;
                                                                                                                                                                  Homo sapiens
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30-MAR-1998;
31-MAR-1998;
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15-APR-1998;
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PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDFEDDICKYDFVEVEEFSDGSVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
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llarity 87.0%; Pred. No. 2.1e-163;
Conservative 27; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Fig 207; 530pp; English
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9805-008358
9805-008358
9805-0084414
9805-0084441
9805-0084647
9805-0084627
9805-0084639
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9805-0085338
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N-PSDB; AAZ34296.
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27; Mismatches

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300; Conservative
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                                                                                LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                             PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
                                  GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                   LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a vascular endothelial growth factor related (VEGF-R) protein. VEGF-R can be used in assays to identify compounds that bind to it or that antagonize its activity. VEGF-R antagonizes (e.g. anti-VEGF-R antagonizes (e.g. anti-VEGF-R antagonizes (e.g. anti-VEGF-R instibution tissue growth. This is useful for inhibiting tissue growth. This is useful for inhibiting transcr. VEGF-R itself can be used to stimulate tissue growth, anglogenesis and to treat coronary artery blockage. The VEGF-R coding sequence can be used for the recombinant production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth factor related protein and related for identifying antagonists and binding
                                                                                                                                                                                                                                                                                                                                      Vascular endothelial growth factor related protein; VEGF-R prot
tissue growth inhibition; tumour growth; cancer; tissue growth;
angiogenesis; coronary artery blockage.
                                                                                                                                                                           VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                  Human vascular endothelial growth factor related protein.
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98US-0072635.
98US-0088089.
98US-0090544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A vascular endothelial polynucleotide, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the VEGF-R protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELIL ) LILLY
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              WO9937671-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JAN-1999;
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05-JUN-1998;
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Length 345;

Score 1667; DB 20; Pred. No. 2.1e-163;

90.2%;

Query Match Best Local Similarity

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                                                            PKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
                                                                                            120
                                                                                                                            GRWCGSGTVPGKQTSKGNHIRIREPVSDEYFPSEPGFCTHYSIIMPQVTETTSPSVLPPSS 180
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                                                                                                                                                121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGECHYNIVMPQFTEAVSPSVLPPSA
                                                                                  61 PREPHTYPRNITVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEBPSDGTIL
                                                                                                                                                                                                             MLLIGLILLITSALAGORTGTRAESNLSSKLOLSSDKEONGVODPRHERVVTISGNGSIHS
               181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                            241 LKBEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor homologs and the nucleic acids that encode them, useful
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10-NOV-1999; 99US-0164463.
04-FEB-2000; 2000US-0180169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human zvegf3, SEQ ID NO:33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-687541/67.
N-PSDB; AAC81582.
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24-MAR-2000; 2000WO-US06427

12-OCT-2000

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cc characterised by a PDGF cystine knot structure, and a CUB domain (AABA8655) which has a beta barrel structure. Zvegf4 has PDGF-like activity, having mitogenic activity on fibroblasts, vascular smooth muscle cells and pericytes, and has also been shown to stimulate bone growth. The invention also relates to fusion proteins comprising human cyceff or fragments thereof, particularly human zvegf4/human zvegf4/human zvegf4 to activations; expression constructs and host cells comprising human zvegf4 cudies or human zvegf4 or a fragment thereof; a method of activating a cell-surface PDGF receptor using a zvegf4-derived polypeptide; a cell-surface PDGF receptor using a zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic zvegf4-derived polypeptides; and a method of detecting a genetic conformality in the zvegf4 gene of a patient. Zvegf4 proteins and derived fragments may be used to stimulate tissue development or repair, or cellular differentiation or proliferation. They are particularly used for the treatment or repair of liver damage, and may also be used to multiple sclerosis). Due to their costeogenic activity, they may also be in the treatment of periodontal disease and fractures. They may also be unded endothelial precursor stem cells, which may be useful in the treatment of ischaemia, in wound healing, and in the modulation of the immune system. The present sequence represents human zvegf3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLLLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
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87.0%; Pred. No. 2.1e-163;
iive 27; Mismatches 18;
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Matches 300; Conservative
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WO200059940-A2 Homo sapiens

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                                                                                                                                                                                                                                                                                                          promoting wound healing or simulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LPB or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LPB antagonist. The method is useful for enhancing itssue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LPB are useful for treating theorem the present sequence represents human LPB, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MILLGILLLTSALAGORTGTRABSNLSSKLOLSSDKEONGVODPRHERVVTISGNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 PKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEPSDGSVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LSLDLINNAVTAFSTLEELIRYLEPDRWOVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                    Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LP8 or its analog and treating atherosclerosis by administering LP8 antagonist
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                                                                                                                                                                                                                                                                                               present invention describes a method for enhancing tissue growth,
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                                                                       99US-0127913
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Best Local Similarity
Matches 300; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                          also called VEGFh.
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tag; detection; cancer.

expressed sequence

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PRFPHTYPRNITVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC78458 to AAC78599 represent polynucleotide and BST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polymerlades. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive using the polypeptides for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78897 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , Baker KP, Botstein D, Desnoyers L, Eaton DL; Filvaroff E, Fong S, Gao W, Gerber H, Gerriten ME; Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ; Kuo SS, Napjer MA, Pan J, Paoni NF, Roy MA; Stewart TA, Tumas D, Williams PM, Wood WI;
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87.0%; Pred. No. 2.1e-163;
iive 27; Mismatches 18;
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                                                                                                                                                                 99US-0123957
99US-0126773
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99US-0131445
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99US-0145698
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99WO-US30095
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06-JAN-2000; 2000WO-US00376
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les 300; Conservative
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Filvaroff E,
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Goddard A, Godowski PJ
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                                                           WO200053756-A2
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06-JAN-2000;
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23-JUN-1999;
26-JUL-1999;
                              Homo sapiens.
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28-APR-1999;
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Shelton DL,
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Gaps

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18; Indels

Length 345;

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antitheumatic, antiathritic, antipacriatic and antidabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                  300
                                                                                                                                                        241 LIEBVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                   GRWCGSGTVPGKÇISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or
preventing diseases associated with inappropriate angiogenesis activity
such as cancer, rheumatoid arthritis, psoriasis and wounds -
                                                                            LSLDLLINNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                    241 LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK
Sprengel JJ, Yon JR, Dijkmans JJH, Gosiewska A;
                                                                                                                                                                                                            VIKKYHEVLOLRPKTGVKGLHKSLTDVALEHHEBCDCVCRGNAGG 345
                                                                                                                                                                                                                                301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human RACE generated VEGF-X protein.
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99US-0124967.
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vascularization. This sequence represents the RACE generated human {\tt VEGF-X} protein described in the method of the invention.
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                                                 Query Match 90.2%; Score 1667; DB 21; Length 345; Best Local Similarity 87.0%; Pred. No. 2.1e-163; Matches 300; Conservative 27; Mismatches 18; Indels 0;
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(c) 1993 - 2003 Compugen Ltd.
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US-08-936-135-6
US-08-872-757-4
US-08-866-650-3
US-09-240-473-3
US-09-240-473-3
US-09-432-473-4
US-09-432-473-4
US-09-432-473-4
US-09-231-408-2
US-09-240-473-5
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Fatent No. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E:
APPLICANT: Shedpard, Pull O.
APPLICANT: Sheppard, Pull O.
APPLICANT: Sheppard, Pull O.
APPLICANT: Sheppard, Pull O.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: West. James W.
TITLE REFERENCE: 98-60
CURRENT FILING DAITE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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3643
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; ORGANISM: Mus musculus
US-09-457-066-43
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CURRENT FILING DATE: 2000-11-06
PRIOR APPLIANG DATE: 18/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTHARE: PASLSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 345
                                                                                                                                                  TYPE: PRT ORGANISM: Mus musculus
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US-09-040-220D-2
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LENGTH: 345
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Best Local S
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  VIKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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Patent No. 6528050
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVATION: GROWTH FACTOR HOMOLOG ZVEGF3; FILE REFERENCE: 98-60C1
; CURRENT APPLICATION NUMBER: US/09/706,968
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GENERAL MO: 07-30-30-00.

APPLICANT: Glabert, Teresa
APPLICANT: Sheppard, Paul O.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REPRENCE: 99-19
CURRENT APPLICATION NUMBER: US 09/364,595D
CURRENT FILING DATE: 2000-05-03
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR FILING DATE: 1999-05-03
FRIOR FILING DATE: 1999-05-03
FRIOR FILING DATE: 1999-05-04
FRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SEQ ID NOS: 57
LINGTH: 345
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                                                                                                            Sequence 35, Application US/09564595D Patent No. 6495668
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Best Local Similarity
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US-09-706-968-43
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Setent No. 6391311
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Forrara, Napoleone
APPLICANT: KNO, SOPHIA S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOWOLOGY TO VASCULAR
TITLE OF INVENTION: BENOTHELIAL CELL GROWH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
FILE REPRESENCE: P1122
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT FILING DATE: 1998-03-17
SEG ID NOS: 8
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Query Match 100.0%; Score 1848; DB 4; Best Local Similarity 100.0%; Pred. No. 7.2e-195; Matches 345; Conservative 0; Mismatches 0;
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61 PRFPHTYPRNTYLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KAO, SOPHIA S.

TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1

FILE REFERENCE: P1122P2

CURRENT APPLICATION NUMBER: US/09/265,686

CURRENT FILING DATE: 1999-03-10

PRIOR FILING DATE: 1998-03-17

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 8

SEQ ID NO S

TYPE: PRT
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Sequence 5, Application US/09540224

Sequence 5, Application US/09540224

Selent No. 6468543

SERICANT: Glibertson, Debra G.

APPLICANT: Glibertson, Debra G.

APPLICANT: Hart, Charles E.

TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

FILE REFERENCE: 00-28

CURRENT APPLICATION NUMBER: US/09/540,224

CURRENT PILING DATE: 2000-03-31

BARLIER APPLICATION NUMBER: US 60/180,169

FARLIER FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5

LENGTH: 345

TYPE: PRT

ORGANISM: Homo sapiens

US-09-540-224-5
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90.2%; Score 1667; DB 4;
Best Local Similarity 87.0%; Pred. No. 6.2e-175;
Matches 300; Conservative 27; Mismatches 18;
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Best Local Similarity 87.0
Matches 300; Conservative
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                                   181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                 US-0015

US-00457-066-2

Sequence 2, Application US/09457066

Patent No. 6432673

GENERAL INFOWATION:

APPLICANT: Gao, Zeren

APPLICANT: Hart, Charles E.

APPLICANT: Piddington, Christopher S.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Gilberson, Debra G.

APPLICANT: Gilberson, Debra G.

FILE REFRENCE: 98-60

FILE REFRENCE: 98-60

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 2.

LENGTH: 345
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US-09-265-686-2
; Sequence 2, Application US/09265686
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Matches 300; Conservative
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; ORGANISM: Homo sapiens
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                                                                             90.2%; Score 1667; DB 4;
87.0%; Pred. No. 6.2e-175;
live 27; Mismatches 18;
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Fatent No. 6495668
GENERAL INFORMATION
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
                                                                                                                                                                                                                                                                                                                                                                               ZVEGF3
                                                                                                                                                                                                                                         APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Shedpard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVE
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2.
                                                                                                                                                                                           Sequence 2, Application US/09706968
Patent No. 6528050
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Best Local Similarity 87.0%
Matches 300; Conservative
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US-09-564-595D-57
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US-09-706-968-2
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                           MILLGLLILITSALAGORTGTRAESNLSSKLOLSSDKEONGVODPRHERVVTISGNGSIHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-564-595D-33
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US-09-564-595D-33
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LENGTH: 345
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                                                                                                                                                                                                                                                           106 YDFVEVEEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDBYFPSEPGFCIHYSIIMP 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 AFLYGKKSKVVNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCA 285
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                                                  Length 302
                                                                                                       Indels
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US-09-564-595D-56
j Sequence 56, Application US/09564595D
j Patent No. 6495668
j GENERAL INFORMATION:
j APPLICANT: Glibert, Teresa
j APPLICANT: Hart, Charles E.
j APPLICANT: Hart, Charles E.
j TITLE OF INVENTION: ROWTH FACTOR HOMOLOG ZVEGF4
j TITLE OF INVENTION: BROWTH FACTOR HOMOLOG ZVEGF4
j FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
j CURRENT FILING DATE: 1999-05-03
pRIOR PILING DATE: 1999-05-03
pRIOR PILING DATE: 1999-11-10
j PRIOR PILING DATE: 1999-11-10
j PRIOR FILING DATE: 2000-02-04
j NUMBER OF SEQ ID NOS: 57
seq ID NO 56
j SEQ ID NO 56
j LENGTH: 317
                                                  64.9%; Score 1200; DB 4; 72.4%; Pred. No. 1.4e-123; iive 35; Mismatches 43;
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                                                  Query Match
Best Local Similarity 72.49
Matches 215; Conservative
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     US-09-564-595D-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 DETIQVKGNGYVQSPRFPNSYPRNLLITWRLHS-QENTRIQLVFDNQFGLEEAENDICRY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 -MPQVTETTSPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 LGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 ERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.2%; Score 1204.5; DB 4; Length
71.3%; Pred. No. 4.5e-124;
.ive 42; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 54, Application US/09564595D; Patent No. 6499668 genuence 54, Application US/09564595D; Patent No. 6499668 genuence 54, Application US/09564595D genuence 54, Application US/09564595D genuence 54, Application Genuence 56, Application Genuence 67, TITLE OF INVENTION: Paul O. TITLE OF INVENTION: GROWTH PACTOR HOMOLOG ZVEGF4; FILE REFERENCE: 99-19 CURRENT APPLICATION NUMBER: US/09/564,595D; CURRENT PILING DATE: 1999-05-03 prior Application NUMBER: US 09/304,216; PRIOR APPLICATION NUMBER: US 09/304,216; PRIOR APPLICATION NUMBER: US 60/164,463; PRIOR APPLICATION NUMBER: US 60/160,169; PRIOR FILING DATE: 1099-11-10; PRIOR FILING DATE: 2000-02-04; NUMBER OF SEQ ID NOS: 57; SOFTWARE: FastSEQ for Windows Version 4.0; LUNG US 54; LUNG 54.
CURRENT APPLICATION NUMBER: US/09/564,595D CURRENT FILING DATE: 2000-05-03 PRIOR APPLICATION NUMBER: US 09/304,216 PRIOR FILING DATE: 1999-05-03 PRIOR PILING DATE: 1999-11-10 PRIOR PELING DATE: 1999-11-10 PRIOR PELING DATE: 1999-11-10 PRIOR PILING DATE: 2000-02-04 NUMBER OF SEQ ID NOS: 57 SOFTWARE: FASTSEQ for Windows Version 4.0
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OTHER INFORMATION: fusion polypeptide
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, OTHER INFORMATION: fusion polypeptide
US-09-564-595D-57
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ORGANISM: Artificial Sequence
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Best Local Similarity 71.34
Matches 216; Conservative
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US-09-564-595D-54
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LENGTH: 303
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RESULT 15
US-09-540-224-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 BDLENMYLDTPRYRGRSY-HDRKSK-VDLDRLNDDAKRYSCTPRNYSVNIREBLKLANVV 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 QVTET-----TSPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQ 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 VDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEBVKLYSCTPRNFSVSIRBELKRTDTI 269
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SWQEDLENMYLDTPRYRGRSY-HDRXSKVVDLNLLTEEVRLYSCTPRNFSVSIREELKRT 238
                                                         DIIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRPKTGVKGLHKSLTD 326
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US-09-564-595D-55
Sequence 55, Application US/09564595D
Patent No. 649568
GENERAL INFORMATION:
APPLICANT: Glibert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR PILING DATE: 1999-05-03
PRIOR PILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-15-03
PRIOR FILING DATE: 1999-16-03
PRIOR FILING DATE: 1999-16-03
SEQUENCE FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SEQ ID NO 55
LEAGTH: 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.1%; Score 1019; DB 4;
60.4%; Pred. No. 1.3e-103;
tive 41; Mismatches 61;
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                                                                                                                                VALEHHEECDCVCRGSTGG 317
                                                                                                            327 VALEHHEECDCVCRGNAGG 345
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ORGANISM: Artificial Sequence
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IQLDHHERCDCIC 310
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Matches 189; Conservative
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US-09-457-066-37
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; Sequence 37, Application US/09457066; Patent No. 6432673; GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

40.7%; Score 752; DB 4; Length 370;
Best Local Similarity 45.3%; Pred. No. 4.3e-74;
Matches 148; Conservative 59; Mismatches 92; Indels
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Fatent No. 6468543

GENERAL INFORMATION:
GENERAL INFORMATION:
FAPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

CURRENT PLICATION NUMBER: US/09/540,224

CURRENT FILING DATE: 2000-03-31

EARLIER FILING DATE: 2000-03-34

EARLIER FILING DATE: 2000-02-04
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly
APPLICANT: Gilbertson, Debra G.
APPLICANT: GROWTH FACTOR HOMOLOG ZVEGF3
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REPERENCE: 99-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT PALLICATION NUMBER: US/09/457,066
CURRENT PILIOR DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: PastSEQ for Windows Version 3.0
IENGTH: 370
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SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 370
TYPE: PRT
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SEQ ID NO 4
LENGTH: 345
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US-09-823-033-4
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Sequence 7, Appli
Sequence 7, Appli
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Sequence 4, Appli
Sequence 2, Appli
Sequence 149, Appli
Sequence 488, Appli
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Sequence 688, Appli
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                                                                                                                                                                                             1848
1 MLLGLLLTSALAGQRTGT ......DVALEHHEECDCVCRGNAGG 345
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2. (cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3. (cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5. (cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6. (cgn2_6/ptodata/1/pubpaa/PUBCOMB.pep:*
7. (cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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7. (cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
7. (cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-978-295A-488
US-09-978-697-488
US-09-978-192A-488
US-09-99-832A-488
US-09-978-189-488
US-09-796-753-6
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US-10-139-583-43
US-10-131-600-7
US-10-264-361-4
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US-09-923-995-4
                                                                                                                                                                                                                                                                                                     673684 seqs, 184443283 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                      protein search, using sw model
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Maximum DB seq length: 200000000
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-09-978-608A-4	-09-978-585A-48	US-09-978-191A-488	-09-978	-09-97	-09-999-833A-48	-09-98	-09-978-	-09-918-5	US-09-978-423A-488	-09-978-193A-48	-48	-09-978-7	-09-978-187B-48	-978-643A-48	-09-978-375A-48	-60-	-09-978-298A-48	US-10-137-870-286	0-140-018-	-10-140-0	-10-140-274-	-10-140-471-	-10-140-807-28	US-10-140-922-286	-10-140-924-28	-10-140-926-28	US-10-141-698-286	-10-141-702-2	US-10-141-704-286
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ALIGNMENTS

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100.0%; Pred. No. 5.8e-174;
tive 0; Mismatches 0;
Sequence 4, Application US/09823033
Sequence 4, Application US/09823033
Patent No. US20020004225A1
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT APPLICATION NUMBER: US/09/823,033
CURRENT APPLICATION NUMBER: US/09/823,033
NUMBER OF SEQ ID MOS: 5
NUMBER OF SEQ ID MOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches 345; Conservative
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61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
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                                                                                        ## APPLICANT: USSIMAN, ALILIA
## APPLICANT: HELDIN, Carl-Henrik
## APPLICANT: HELDIN, Carl-Henrik
## APPLICANT: HELDIN, Carl-Henrik
## APPLICANT: HERREOUZ, Christer
## ITILE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
## ITILE OF INVENTION: THEREFOR, AND USES THEREOF
## ITILE OF INVENTION: 09-410349-Eriksson et al-1064-44740
## CURRENT APPLICATION NUMBER: US/09/852,209A
## CURRENT APPLICATION NUMBER: 09/410,349
## RIOR APPLICATION NUMBER: 60/110,749
## RIOR FILING DATE: 1999-09-30
## PRIOR APPLICATION NUMBER: 60/113,002
## PRIOR APPLICATION NUMBER: 60/113,002
## RROR APPLICATION NUMBER: 60/135,426
## RROR APPLICATION NUMBER: 60/135,426
## RROR APPLICATION NUMBER: 60/144,022
## RROR APPLICATION NUMBER: 60/144,022
## RROR PRILING DATE: 1999-05-21
## RROR PILING DATE: 1999-07-15
## NUMBER OF SEQ ID NOS: 39
## SEQ ID NOS: 39
## SEQ ID NOS: 39
## SEQ ID NOS: 39
## SEQ ID NOS: 39
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FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/10/139,583
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, Sequence 43, Application US/10139583
Publication No. US20020177193A1
, GENERAL INFORMATION:
, APPLICANT: Gao, Zeren
, APPLICANT: Hart, Charles E.
, APPLICANT: Piddington, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 345; Conservative
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US-09-852-209A-7
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Sequence 2, Application US/09818943

Sequence 2, Application US/09818943

GENERAL INFORMATION:

APPLICANT: ENERGSON, U1f

APPLICANT: PONTEN, Annica

APPLICANT: AASE, Karin

APPLICANT: ALI, Hong

TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F

TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F

TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F

TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F

TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F

TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH F

TITLE OF INVENTION NUMBER: US/09/818,943

CURRENT FILING DATE: 2001-03-28

PRIOR FILING DATE: 2000-03-28

NUMBER OF SEQ ID NOS: 7

SOUTHWARE: PATCHIN VERSION 3.0
                                                                                  241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNBCQCVPRK 300
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Patent No. US20020164687A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, UIF
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | SEQ ID NO 2 | LENGTH: 345 | TYPE: PRT | ORGANISM: Murinae gen. sp. US-09-818-943-2
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Matches 345; Conservative
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US-09-852-209A-7
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US-09-818-943-2
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                                                                                                                                               100.0%; Score 1848; DB 15; Length 345; 100.0%; Pred. No. 5.8e-174;
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100.0%; Pred. No. 5.8e-174;
Live 0; Mismatches 0; Indels 0;
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Fublication No. US20030087870A1
GENERAL INFORMATION.
APPLICATION NO. US20030087870A1
GENERAL INFORMATION.
TITLE OF INVENTION: METHOD OF TREATING FIBROSIS
FILE REFERENCE: 00-53
CURRENT FILING DATE: 2002-10-03
FRIOR APPLICATION NUMBER: US/09/695,121
FRIOR APPLICATION NUMBER: US/09/695,121
FRIOR PRIOR DATE: 2000-10-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTESEQ for Windows Version 3.0
                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                      Best Local Similarity 100.0
Matches 345; Conservative
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Best Local Similarity 100.
Matches 345; Conservative
                                                 TYPE: PRT

ORGANISM: Murinae gen. sp.
US-10-131-600-7
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    SEQ ID NO 7
LENGTH: 345
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US-10-264-361-4
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APPLICANT: AASE, KALI
APPLICANT: LEE, XULI
APPLICANT: DONTEN, Marica
APPLICANT: PONTEN, Marko
APPLICANT: PONTEN, Marko
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: BETSHOLTZ, Christer
TITLE OF INVENTION: PLAISLE-DERIVED GROWTH FACTOR C, D
TITLE OF INVENTION: PLAISLE-DERIVED GROWTH FACTOR C, D
TITLE OF INVENTION: PLAISLE-DERIVED GROWTH FACTOR C, D
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TITLE OF INVENTION: PLAISLE-DERIVED GROWTH FACTOR C, D
TITLE OF INVENTION: PLAISLE-DERIVED GROWTH FACTOR C, D
TITLE OF INVENTION NUMBER: US/09/410,349
FRIOR APPLICATION NUMBER: 60/10,109
FRIOR FILING DATE: 1998-11-12
FRIOR FILING DATE: 1998-12-18
FRIOR FILING DATE: 1998-12-18
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-05-21
FRIOR FILING DATE: 1999-07-15
NUMBER: OF SEQ. ID NOS: 39
SOFTWARE: PATCHTIN VET. 2.0
                                                                                                                                                                                                                                                            100.0%; Score 1848; DB 14;
100.0%; Pred. No. 5.8e-174;
Live 0; Mismatches 0; 1
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: 09/457,066
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASISEQ for Windows Version 3.0
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Sequence 7, Application US/10131600

Publication No. US20030082670A1

GENERAL INFORMATION:

APPLICANT: ERIXSSON, Ulf
                                                                                                                                                                                                                                                                                                              Matches 345; Conservative
                                                                                                                                                                 TYPE: PRT
CORGANISM: Mus musculus
US-10-139-583-43
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Best Local Similarity
                                                                                                                    SEQ ID NO 43
LENGTH: 345
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 345 LTYPE: PRT ORGANISM: Homo sapiens
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Matches 300; Conservative
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US-09-795-006A-149
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US-09-795-006A-149
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90.2%; Score 1667; DB 9; Length 345;
Best Local Similarity 87.0%; Pred. No. 4.5e-156;
Matches 300; Conservative 27; Mismatches 18; Indels
                                                                                                                                                                                          RESULT 7
US-09-823-033-2
i Sequence 2, Application US/09823033
j Sequence 2, Application US/09823033
j Patent No. US20020004225A1
j GENERAL INFORMATION:
    APPLICANT: Hart, Charles E.
    APPLICANT: Gilbertson, Debra G.
    TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
    TITLE OF INVENTION: LIGAMENT AND CARTILAGE
    TITLE OF INVENTION: LIGAMENT AND CARTILAGE
    CURRENT APPLICATION NUMBER: US/09/823,033
    CURRENT FILING DATE: 2001-03-29
    NUMBER OF SEQ ID NOS: 5
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 2
    LENGTH: 345
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                                                                                                                             301 VIKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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; Patent No. US2020081700A1
; GENERAL INFORMATION:
; APPLICANT Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1; FILLE REFERENCE: 00-47
; CURRENT APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/223,164
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
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US-09-823-033-2
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US-09-923-995-4
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FREENT NO. USZOUZO151680A1
GENERAL INFORMATION:
HAPPLICANT. Alitalo et al
FILLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
FILLE OF INVENTION: ENDOTHBLIAL GROWTH FACTOR DNAS AND PROTEINS
FILLE REFERENCE. 28967/359778
CURRENT APPLICATION NUMBER: US/09/795,006A
CURRENT PLING DATE: 2001-02-26
FRIOR PAPLICATION NUMBER: US 60/205,331
FRIOR FILING DATE: 2000-05-18
FRIOR FILING DATE: 2000-05-25
NUMBER OF SEQ ID NOS: 175
SOFTWARE: Parentin Ver: 2.0
IEBNGTH: 345
                                                                                                                  1 MILLGLILLTSALAGQRIGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS
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90.2%; Score 1667; DB 9; Length 345; 87.0%; Pred. No. 4.5e-156;
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PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR PILING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR APPLICATION NUMBER: 60/08195
PRIOR APPLICATION NUMBER: 60/081952
PRIOR PELING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR PILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR APPLICATION NUMBER: 60/082568
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PRIOR PILING DATE: 1998-04-21
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R APPLICATION NUMBER: 60/080107

R APPLICATION NUMBER: 60/080165

R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080397

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080328

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080338

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080334

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080334

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/080334

R FILING DATE: 1998-04-01

R APPLICATION NUMBER: 60/08034

R FILING DATE: 1998-04-01
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R APPLICATION NUMBER: 60/081229
R APPLICATION NUMBER: 60/081955
R APPLICATION NUMBER: 60/081955
R FILING DATE: 1998-04-15
R PILING DATE: 1998-04-15
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R FILING DATE: 1998-03-25
R FILING DATE: 1998-03-26
R FILING DATE: 1998-03-26
R APPLICATION NUMBER: 60/079664
R FILING DATE: 1998-03-27
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R APPLICATION NUMBER: 60/079728
R PILING DATE: 1998-03-27
R FILING DATE: 1998-03-27
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R FILING DATE: 1998-03-27
R FILING DATE: 1998-03-7
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R FILING DATE: 1998-04-08
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R FILING DATE: 1998-04-08
                APPLICATION NUMBER: 60/078886
FILING DATE: 1998-03-20
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APPLICATION UNDERS: 60/078910
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078939
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PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
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APPLICATION NUMBER: 60/080105
   FILING DATE: 1998-03-13
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APPLICANT:

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same TITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/978,295A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 60/062250

PRIOR PILING DATE: 1997-10-17

PRIOR PILING DATE: 1997-11-3

PRIOR PILING DATE: 1997-11-3

PRIOR APPLICATION NUMBER: 60/06344

PRIOR PILING DATE: 1997-11-3

PRIOR APPLICATION NUMBER: 60/07450

PRIOR APPLICATION NUMBER: 60/077450

PRIOR APPLICATION NUMBER: 60/077450

PRIOR APPLICATION NUMBER: 60/077491

PRIOR PILING DATE: 1998-03-11

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                                                                                                                                                                                    241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
121 GRWCGSGTVPGKQISKGNQIRIRFVSDBYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Godwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Patent No. US20020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Botstein, David
Desnoyers, Luc
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Kuo, Sophia S.
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US-09-978-295A-488
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R APPLICATION NUMBER: 60/082700
R FILING DATE: 1998-04-22
R PAPLICATION NUMBER: 60/082797
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082796
R FILING DATE: 1998-04-23
R APPLICATION NUMBER: 60/08336
R FILING DATE: 1998-04-27
R APPLICATION NUMBER: 60/083322
R FILING DATE: 1998-04-28
R APPLICATION NUMBER: 60/08392
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R APPLICATION NUMBER: 60/08392
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R RAPLICATION NUMBER: 60/083554
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R RILING DATE: 1998-05-06
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R RAPLICATION NUMBER: 60/084639
R RAPLICATION NUMBER: 60/084640
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R RAPLICATION NUMBER: 60/084598
R RAPLICATION NUMBER: 60/08459
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RR FILING DATE: 1998-05-15
RR APPLICATION NUMBER: 60/085579
RR FILING DATE: 1998-05-15
RR APPLICATION NUMBER: 60/085580
RR FILING DATE: 1998-05-15
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R APPLICATION NUMBER: 60/083496
R FILING DATE: 1998-04-29
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
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APPLICATION UNMBER: 60/085582
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085704
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/084414
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APPLICATION NUMBER: 60/085323
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                                                        1 MILLIGILLITSALAGORTGTRAESNISSKLOLSSDKEONGVODPRHERVVTISGNGSIHS 60
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams P. Mickey
APPLICANT: Williams P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC27
CURRENT PELLION: ACIDS CON1-10-16
PRIOR FILING DATE: 2001-10-16
PRIOR PLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
                                                                                1 MSLFGLLLLTSALAGQRQCTQAESNLSSKRQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                            61 PREPHTYPRNITYLVHRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEVEVEBPSDGILL
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                     Indels
                       18;
; Pred. No. 4.5e-156; 27; Mismatches 18;
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Sequence 488, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/064249
FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
87.0%;
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Gao, Wei-Qiang
Gerber, Hanspeter
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Filvaroff, Ellen
Best Local Similarity 87.0%
Matches 300; Conservative
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Kuo, Sophia S.
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Pan, James;
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APPLICANT: Baker Kevin P.
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR APPLICATION NUMBER: 60/08268
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PRIOR PLING DATE: 1998-04-27
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INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same
                                    TITLE OR TAVARALINE, ACIDS EMOCATING THE SAME
FILE REFERENCE: P263.0PLC9
CURRENT PLINIG DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 05/918585
PRIOR PLINIG DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 06/062260
PRIOR APPLICATION NUMBER: 06/062260
PRIOR PLINIG DATE: 1997-11-13
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FILING DATE: 1998-04-08
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
  PRIOR APPLICATION NUMBER: 60/085689
PRIOR PILING DATE: 1998-05-15
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PRIOR PILING DATE: 1998-05-15
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PRIOR PILING DATE: 1998-05-15
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Patent No. US20020177553A1
GENERAL INFORMATION:
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Filvaroff, Ellen
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APPLICANT: Baker Kevin P.
APPLICANT: Botsein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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Kuo, Sophia S.
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PRIOR PELICATION NUMBER: 60/081195
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NR APPLICATION NUMBER: 60/081955
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241 LKEEVKLYSCTPRINESVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300 241 LTBEVRLYSCTPRNFSVSIRBELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180 1 MLLLGLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS LSLDLLNNAVTAFSTLBELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL Gaps .. 0 Length 345; 301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345 VTKKYHEVLOLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345 Indels Query Match 90.2%; Score 1667; DB 10; Best Local Similarity 87.0%; Pred. No. 4.5e-156; Matches 300; Conservative 27; Mismatches 18; PRIOR APPLICATION NUMBER: 60/084643
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PRIOR PLING DATE: 1998-05-15 Sequence 488, Application US/0999832A Publication No. US20020192706A1 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David Godowski, Paul J. Grimaldi, J. Christopher Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Ferrara, Napoleon Filvaroff, Ellen DATE: 1998-05-07 Goddard, Audrey Desnoyers, Luc Eaton, Dan US-09-999-832A-488 APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: 61 121 181 301 APPLICANT: APPLICANT: APPLICANT: 셤 셤 à 요 ò 셤 à ద à à ò

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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
Gurney, Austin L.
Hillan, Kenneth J
                                      Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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APPLICANT: Tunas, Daniel
APPLICANT: Tunas, Daniel
APPLICANT: Williams, Daniel
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TITLE OF INVENTION: Accepted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: PS610PL7-15
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E
Baker Kevin P.
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Desnoyers, Luc
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Sequence 488, Application US/09978189 Publication No. US20030004102A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi

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241 LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                   | Sequence 6, Application US/09796753 | Publication No. US2030027998A1 |
| Publication No. US2030027998A1 |
| Publication No. US2030302799A1 |
| Publication No. US2030302799A1 |
| Publication No. US203030279A1 |
| TILLE REFERENCE: 7532.227-99 |
| CURRENT APPLICATION NUMBER: US/09/796,753 |
| CURRENT APPLICATION NUMBER: US/09/796,753 |
| PRIOR PRINKS DATE: 1098-10-30 |
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241 LKBEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300 241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                         61 PKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
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                                                                                                                                             1 MSLFGLLLLTSALAGQRQGTQAESNLSSKRQFSSNKEQNGVQDPQHERLITVSTNGSIHS
                                                                                                              1 MILLGILLITSALAGORIGIRAESNISSKLOLSSDKEQNGVODPRHERVVTISGNGSIHS
                                                         0; Gaps
90.2%; Score 1667; DB 11; Length 345; 87.0%; Pred. No. 4.5e-156; tive 27; Mismatches 18; Indels 0;
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  Query Match
Best Local Similarity 87.0%
Matches 300; Conservative
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Sequence 4, Appli Sequence 43, Appl Sequence 2, Appli

Sequence

Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 4, Appli Sequence 286, App Sequence 286, App Sequence 2, Appli

OM protein

on:

Sequence:

Searched:

Database

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APPLICANT: LUNGERATION:
APPLICANT: LUNGER INSTITUTE FOR CANCER RESEARCH
APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.
TITLE OF INVENTION: PLATELET-DERAVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REPERRICE: PCT/US99/22669 LUDWIG INST FOR CANCER
CURRENT APPLICATION NUMBER: PCT/US99/22668B
CURRENT FILING DATE: 1999-09-30
EARLIER FILING DATE: 1998-09-30
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-12-03
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EARLIER FILING DATE: 1998-12-18
EARLIER FILING DATE: 1998-05-21
EARLIER APPLICATION NUMBER: 60/113,426
EARLIER FILING DATE: 1999-05-21
EARLIER FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
8 US-09-304-216-35

8 US-09-410-7434-7

9 US-09-5410-7434-7

9 US-09-5410-752-43

1 US-09-695-121-4

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                                                                                     ULH HILLHHILLHHIN BOD HOR A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G B A G 
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1852.926 Million cell updates/sec
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                                                                                                                                               November 25, 2003, 21:02:19; Search time 169.42 Seconds
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1 MLLIGLILLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG
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                               GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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                                                 Copyright
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Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 51,

Sequence 6, Appl

Sequence Sequence Sequence Sequence

Sequence

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Result Š.

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301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Murinae gen. sp.
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Best Local Similarity 100.0%; Pred. No. 3.2e-175;
Matches 345; Conservative 0; Mismatches 0; Indels 0; Gaps
                                                                                                                                                                                       0; Gaps
                                                                                                                                  100.0%; Score 1848; DB 1; Length 345; 100.0%; Pred. No. 3.2e-175; tive 0; Mismatches 0; Indels 0;
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APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF4
FILE REPERENCE: 99-19X
CURRENT APPLICATION NUMBER: US/09/304,216
CURRENT FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 35, Application US/09304216; GENERAL INFORMATION:
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                     Matches 345; Conservative
                                                                                 ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Mus musculus
US-09-304-216-35
                                                                                                                                               Query Match
Best Local Similarity
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LENGTH: 345
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                                                                                                      CT-US99-22668-7
                                       345
                                                              TYPE: PRT
             SEQ ID NO 7
LENGTH: 34
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61 PKFPHTYPRNMYLVMRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFERSDGSVL 120
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                                                                      241 LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                             241 LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECOCVPRK 300
181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 240
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APPLICANT: ASSE, Karin
APPLICANT: LEE, Xuri
APPLICANT: UVIELA, Marko
APPLICANT: UVIELA, Marko
APPLICANT: UVIELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: ALITALO, Kari
APPLICANT: HETSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DI
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DI
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DI
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DI
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C, DI
TITLE OF INVENTION: 1999-09-30
CURRENT APPLICATION NUMBER: 06/108,109
PRIOR FILING DATE: 1999-10-30
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
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                                                                       Sequence 4 Application US/09540703;
GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE;
FILE REPRENCE: 00-12X;
CURRENT APPLICATION NUMBER: US/09/540,703
CURRENT PILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 345
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301 VIKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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100.0%; Pred. No. 3.2e-175;
iive 0; Mismatches 0;
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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT APPLICATION NUMBER: US/09/541,752
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.
Matches 345; Conservative
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; ORGANISM: Mus musculus
US-09-541-752-43
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US-09-540-703-4
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                                                                                                                       1 MLLLGLLLLTSALAGQRTGTRAESNLSSKQQLSSDKEQNGVQDPRHERVVTISGNGSIHS
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Query Match 100.0%; Score 1848; DB 19; Length 345; Best Local Similarity 100.0%; Pred. No. 3.2e-175; Matches 345; Conservative 0; Mismatches 0; Indels 0;
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GENERAL INFORMATION:
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: METHOD OF TREATING FIBROSIS;
FILE REPERENCE: 00-53
CURRENT APPLICATION NUMBER: US/09/695,121
CURRENT FILING DATE: 200-10-23
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
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Best Local Similarity 100.0
Matches 345; Conservative
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TYPE: PRT
ORGANISM: Mus musculus
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US-09-695-121-4
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                                                                                                                                                                 100.0%; Score 1840; DB 23; Length 345; 100.0%; Pred. No. 3.2e-175; ative 0; Mismatches 0; Indels 0;
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100.0%; Pred. No. 3.2e-175;
iive 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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Best Local Similarity 100.
Matches 345; Conservative
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Best Local Similarity 100.
Matches 345; Conservative
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TYPE: PRT
ORGANISM: Mus musculus
                                                                                                         , ORGANISM: Murinae gen.
US-09-818-943-2
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                                                                                         TYPE: PRT
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Sequence 2, Application US/09818943
GENERAL INFORMATION:
APPLICANT: ELI, XUIT
APPLICANT: DI, Annica
APPLICANT: PONTEN, Annica
APPLICANT: ASE, Karin
APPLICANT: LI, Hong
TITLE OF INVENTION: (PDGF-C) AND USES THEREOF
FILE REFERENCE: 1064/48487
CURRENT APPLICATION NUMBER: US/09/818,943
CURRENT PILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-28
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Best Local Similarity 100.0%; Score 1848; DB 21; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.2e-175;
Matches 345; Conservative 0; Mismatches 0; Indels 0:
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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shepmaker, Kimberly E.
APPLICANT: Shemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
TILLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
TILLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
TILLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
TILLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
TILLE OF INVENTION NUMBER: US/09/706,968
CURRENT FILING DAPLICATION NUMBER: US/09/541,752
PRIOR FILING DAPLICATION NUMBER: US/09/541,752
PRIOR FILING DAPLE: 2000-13-31
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 43
LENGTH: 345
                                                                                                                    ; Sequence 43, Application US/09706968; GENERAL INFORMATION:
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ORGANISM: Mus musculus
US-09-706-968-43
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RESULT 12
US-10-131-600-7
Sequence 7, Application US/10131600
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 345; Conservative
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                                                                                                              RESULT 11
US-09-852-209A-7
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LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
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                                                                                                                                                                                             301 VTKKYHEVLOLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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GENERAL INFORMATION:
APPLICANT: BRIKSSON, Ulf
APPLICANT: BRIKSSON, Ulf
APPLICANT: BRIKSSON, Ulf
APPLICANT: BRIKSSON, Ulf
APPLICANT: BRIKSSON, Ulf
APPLICANT: BRIKSSON, Ulf
APPLICANT: DONTEN, Annica
APPLICANT: UUTELE, Kuxi
APPLICANT: UTTALO, Kaxi
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
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APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICANT: HELDIN, Cari-Henrik
APPLICATION NUMBER: US/09/852,209
CURRENT FILING DATE: 1998-09-30
PRIOR FILING DATE: 1998-09-30
PRIOR PELICATION NUMBER: 60/113,002
PRIOR PELICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1998-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR PRIOR APPLICATION NUMBER: 60/144,022
PRIOR FILING DATE: 1999-07-15
PRIOR PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PRIOR DATE: 1999-07-15
PRIOR PRIOR APPLICATION NUMBER: 60/113,002
PRIOR PRIOR APPLICATION NUMBER: 60/113,002
PRIOR PRIOR DATE: 1999-07-15
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Matches 345; Conservative
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; ORGANISM: Murinae gen. sp.
US-09-852-209-7
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US-09-852-209-7
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301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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                                                                                                                                                      Sequence 7, Application US/09852209A
; Sequence 7, Application US/09852209A
; GENERAL INFORMATION:
; APPLICANT: ERIESON, U1f
; APPLICANT: DEE, Xuri
; APPLICANT: UUTEA, MAINICA
; APPLICANT: UUTEA, MAINICA
; APPLICANT: UUTEA, MAINICA
; APPLICANT: ULITALO, KATI
; APPLICANT: BETSHOLTZ, Christer
; APPLICANT: BETSHOLTZ, Christer
; ITILE OF INVENTION: THEREFOR, AND USES THEREOF
; ITILE OF INVENTION: THEREFOR, AND USES THEREOF
; ITILE OF INVENTION: THEREFOR, AND USES THEREOF
; ITILE OF INVENTION: THEREFOR, AND USES THEREOF
; ITILE OF INVENTION: THEREFOR, AND USES THEREOF
; ITILE OF INVENTION: THEREFOR, AND USES THEREOF
; ITILE OF INVENTION: THEREFOR, AND USES THEREOF
; ITILE OF INVENTION UNMBER: 09/410,349
; RIOR PELICATION NUMBER: 60/110,749
; RIOR FILING DATE: 1999-09-30
; PRIOR PELICATION NUMBER: 60/113,002
; PRIOR FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1999-07-15
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PATENTIN VEY: 2.0
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                                                                                                                                            PLICANT: OUTSAN, GATA
PLICANT: ALITALO, KATA
PLICANT: ALITALO, KATA
PLICANT: ALITALO, CARI-Henrik
PLICANT: HELDIN, CARI-HENRIK
PLICANT: HERDIN, CARI-HENRIK
PLICANT: HERDIN, CARI-HENRIK
PLICANT: HERDIN, PLANELET-DERIVED GROWTH FACTOR C, TILE OF INVENTION: PLANELET-DERIVED GROWTH FACTOR C, TILE OF INVENTION: PLANEER: AND USES THEREOF
ILE REFERENCE: 09-410349-ERIKASON et al.1064-44740
JRRENT FILING DATE: 1999-09-30
RIOR APPLICATION NUMBER: US/09/410,349
RIOR RILING DATE: 1998-12-18
RIOR FILING DATE: 1998-12-18
RIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
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PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR PRIOR PRICATION NUMBER: 60/134,022
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1999-07-15
PRIOR FILING DATE: 1990-07-15
PRIOR FILING DATE: 1990-07-15
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                                                                                             PONTEN, Annica
UUTELA, Marko
ERIKSSON, Ulf
AASE, Karin
LEE, Xuri
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APPLICANT: Gao, Zeren APPLICANT: Hart, Charles E. APPLICANT: Piddington, Christopher S. APPLICANT: Sheppard, Paul O. APPLICANT: Shoemaker, Kimberly E. APPLICANT: Gilbertson, Debra G.

APPLICANT: APPLICANT: APPLICANT:

; Sequence 43, Application US/10139583; GENERAL INFORMATION:

US-10-139-583-43

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61 PKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GRWCGSGTVPGKQTSKGNHIRIRFVSDBYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 1848; DB 27; Length 345;
Best Local Similarity 100.0%; Pred. No. 3.2e-175;
Matches 345; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 VIKKYHEVLÖLRPKTGVKGLHKSLIDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 90-60
CURRENT APPLICATION NUMBER: US/10/139,583
CURRENT PILING DATE: 200-50-20
FRIOR APPLICATION NUMBER: 09/457,066
PRIOR PILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 43
LENGTH: 345
TYPE: FRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-264-361-4

Sequence 4. Application US/10264361

SEQUENCE 4. Application US/10264361

SEQUENCE 4. Application.

PEPLICANT: Gilbertsen. Debra G.

TITLE OF INVENTION: METHOD OF TREATING FIBROSIS

TITLE OF INVENTION: METHOD OF TREATING FIBROSIS

CURRENT FAPLICATION NUMBER: US/10/264,361

CURRENT FILING DATE: 2002-10-03

PRIOR FILING DATE: 2001-10-23

NUMBER OF SEQ ID NOS: 18

SEQ ID NO 4

SEQ ID NO 4

SEQ ID NO 4

SEQ ID NO 4

SEQ ID NO 4

SEQ ID NO 4
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Sequence 7. Application US/1030397B

Sequence 7. Application US/1030397B

SEREAL INFORMATION:

APPLICANT: LI, Xuri

APPLICANT: CARMELIET, Peter

APPLICANT: COLUM, Desire

ITILE OF INVENTION: COMPOSITION AND METHOD FOR MODULATING VASCULOGENESIS AND ANGIOGEN

FILE REFERENCE: 2020-11-26

CURRENT PELING DATE: 2090-544/40.23

FURRENT PELING DATE: 1999-09-30

CURRENT PELING DATE: 1999-09-30

PRIOR FILING DATE: 1999-09-30

PRIOR PELICATION NUMBER: US 60/102/461

PRIOR APPLICATION NUMBER: US 60/108, 109

PRIOR PELING DATE: 1998-12-13

PRIOR APPLICATION NUMBER: US 60/110, 749

PRIOR PELING DATE: 1998-12-18

PRIOR PELING DATE: 1998-12-24

PRIOR APPLICATION NUMBER: US 60/113, 002

PRIOR FILING DATE: 1998-12-18

PRIOR PELING DATE: 1999-05-21

PRIOR PELING DATE: 1999-05-21

PRIOR PELING DATE: 1999-07-15

PRIOR PELING DATE: 1999-07-15

PRIOR PELING DATE: 1999-07-15

PRIOR PELING DATE: 1999-07-15

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PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEBPSDGSVL 120
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Best Local Similarity 100.0
Matches 345; Conservative
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; TYPE: PRT
; ORGANISM: Murinae gen. sp.
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'G912_6/ptodata11/paa/USO7_NEW_COMB.pep:*
'G912_6/ptodata11/paa/USO8_NEW_COMB.pep:*
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'G912_6/ptodata11/paa/USO8_NEW_COMB.pep:*
'G912_6/ptodata11/paa/USO8_NEW_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF93
FILE REFERENCE: 98-60
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO.
SEQ ID NO.
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87.0%; Pred. No. 1.5e-136;
iive 27; Mismatches 18;
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87.0%; Pred. No. 1.5e-136;
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SOFTWARE: Patentin version 3.2
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Matches 300; Conservative
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PCT-US03-26491-191
                       SEQ ID NO 191
LENGTH: 345
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Sequence 191, Application PC/TUS0326491

Sequence 191, Application PC/TUS0326491

Sequence 191, Application PC/TUS0326491

Sequence 191, Application PC/TUS0326491

TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR FILE REFERENCE: DO273 PCT

CURRENT APPLICATION NUMBER: PCT/US03/26491

CURRENT FILING DATE: 2003-08-26

PRIOR FILING DATE: 2002-08-27

NUMBER OF SEQ ID NOS: 557
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     VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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                                                                                                                  US-09-876-813-35

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVE
TITLE REFERENCE: 99-19
CURRENT FILING DATE: 2001-06-06
PRIOR PRIOR PAPLICATION NUMBER: US/09/876,813
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 1999-05-03
PRIOR PILING DATE: 1999-05-03
PRIOR PILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-10-07
PRIOR PILING DATE: 1999-10-03
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
PRIOR PILING DATE: 1999-10-05
SPRIOR PILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FESTERE for Windows Version 4.0
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US-09-876-813-35
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Best Local Similarity
Matches 345; Conserv
                                                                               RESULT 2
US-09-876-813-35
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Sequence 191, Application US/10648593 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
US-10-648-593-191
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ORGANISM: Homo sapiens
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 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                                     1 MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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                                  LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVNINL
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                                                                                                                                                                                                                                                                                       Sequence 33, Application US/09876813

GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/876,813
CURRENT FILING DATE: 2001-06-06
PRIOR PILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-013
PRIOR FILING DATE: 1999-013
PRIOR FILING DATE: 1999-011-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
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US-09-876-813-33
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US-09-876-813-33
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Best Local S
Matches 300
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RESULT 6 US-10~648-593-191

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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THA
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THA
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASE AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP
CURRENT APPLICATION UNMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
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TITLE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
FILE REFERENCE: JAB 1687
CURRENT APPLICATION NUMBER: US/10/471,221
CURRENT PILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: US 60/274901
PRIOR PILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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US-10-471-221-1
; Sequence 1, Application US/10471221
; GENERAL INFORMATION:
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Best Local Similarity 87.0%,
Matches 300; Conservative
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US-09-830-320A-4
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APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUMAG, HORGILL
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT APPLICATION NUMBER: US/60/487,610
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1644
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                                                                                                                    GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEFBBGGSVL 120
                                                   GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS 180
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87.0%; Pred. No. 1.5e-136;
iive 27; Mismatches 18;
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Best Local Similarity 87.0
Matches 300; Conservative
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RESULT 9

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APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GRNETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT APPLICATION NUMBER: 0503-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 1042
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APPLICANT: HILMAN, Jennifer L.
APPLICANT: CORLEY, New J.
APPLICANT: CORLEY, New J.
APPLICANT: CORLEY, New J.
APPLICANT: GURGLER, New J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AU-YOUNG, Janice K.
TITLE OF INVENTION: GROWTH FACTOR RELATED MOLECULES
FILE REPERENCE: PF-0627 USN
CURRENT APPLICATION NUMBER: US/09/830,320A
CURRENT FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 60/183,024
PRIOR APPLICATION NUMBER: US 60/155,216
PRIOR APPLICATION NUMBER: US 60/155,216
PRIOR APPLICATION NUMBER: US 60/155,216
PRIOR APPLICATION NUMBER: US 60/155,216
PRIOR APPLICATION NUMBER: US 60/155,216
PRIOR APPLICATION NUMBER: US 60/172,233
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Sequence 1042, Application US/60485450
GENERAL INFORMATION:
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APPLICANT: INCYTE GENOMICS, INC.
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US-60-485-450-1042
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343 AGG 345
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US-09-876-813-57
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GENERAL INFORMATION:
GENERAL INFORMATION:
TATULE OF INVENTION: Modulation Of Smooth Muscle Cell Proliferation
FILE REFERENCE: JAB 1687
CURRENT APPLICATION NUMBER: US,10/471,221
CURRENT FILING DATE: 2003-09-05
PRIOR APPLICATION NUMBER: US 60/274901
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
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86.7%; Pred. No. 7.6e-136;
ive 27; Mismatches 19; Indels
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                                                                                                 ; NAME/KEY: misc feature
; CTHER INFORMATION: Incyte ID No.: 4163378CD1
US-09-830-320A-4
                                                                                                                                                           Query Match
Best Local Similarity 86.7%
Matches 299; Conservative
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NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL Program
SEQ ID NO 4
LENGTH: 345
                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 28
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                                                        181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DETIQVKGNGYVQSPRFPNSYPRNLLLTHWRLHS-QENTRIQLVFDNQFGLEEAENDICRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 -MPQVTETTSPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 DFQPAAASVSPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQL
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                                                                                                                                                                                                                                                                                                       301 VTKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
                                                                                                                                                                                                                                                                                                                                    244 -----BVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
FAPLICANT: Gilbert, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVER
FILLE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/864,595
FRIOR FILING DATE: 2001-06-06
FRIOR APPLICATION NUMBER: US/09/564,595
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 09/304,216
FRIOR APPLICATION NUMBER: US 09/304,106
FRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
LENGRHAR: FastSEQ for Windows Version 4.0
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: fusion polypeptide US-09-876-813-57
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ORGANISM: Artificial Sequence
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SEQ ID NO 56
LENGTH: 317
                                  305
                                                                                                     PCT-US00-28803-7
                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 OVTETTSPSVLPPSSLSLDLLNNAVTARSTLEBLIRYLEPDRWQVDLDSLYKPTWQLLGK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 AFLYGKKSKVVNLNLLKEEVKLYSCTPRNFSVSIREBLKRTDTIFWPGCLLVKRCGGNCA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 YDFVEVERPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCHYSIIMP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HERIITVSINGSIHSPRFPHTYPRNTVLVMRLVAVEENVWIQLTFDERFGLEDPEDDICK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 CCLHNCNECQCVPRKVTKKYHEVLQLRP---KTGVKGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 CGTVNWRSCTCNSGKTVKKYHEVLQFEPGHIKRRGRAKTWALVDIQLDHHERCDCIC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DOLOGO, GRACEL
APPLICANT: Nondo, Gracel
APPLICANT: Nondo, Gracel
APPLICANT: Nondo, Michael
APPLICANT: Hibbun, Erin
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Proteins and Polynucleotides
TITLE OF INVENTION: Brooding the Same
FILE REFERENCE: LEX-0070-PCT
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 60/160,106
PRIOR APPLICATION NUMBER: US 60/160,106
PRIOR APPLICATION NUMBER: US 60/160,106
PRIOR APPLICATION NUMBER: US 60/162,547
PRIOR FILING DATE: 1999-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

64.9%; Score 1200; DB 5; Length 302;
Best Local Similarity 72.4%; Pred. No. 3.6e-96;
Matches 215; Conservative 35; Mismatches 43; Indels
                                                         APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Shepard, Bul O.
TITLE OF INVENTION: GROWTH PACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT PAPLICATION NUMBER: US/09/876,813
CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US/09/564,595
PRIOR PILING DATE: 2000-05-03
PRIOR PILING DATE: 1999-06-03
PRIOR PILING DATE: 1999-06-03
PRIOR PILING DATE: 1999-06-03
PRIOR FILING DATE: 1099-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-04
SOFTWARE FEASEQ FOR WINGOWS VERSION 4.0
SCOTTWARE FEASEQ FOR WINGOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CTHER INFORMATION: fusion polypeptide US-09-876-813-54
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              ; Sequence 54, Application US/09876813; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US00-28803-7
US-09-876-813-54
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121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSFSVLPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 ERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKY 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DFVEVEDISETSTIIRGRWCGHKEVPPRIKSRTNQIKITFKSDDYFVAKPGFKIYYSLLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 PKFPHTYPRNMYLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGSVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PRFPHTYPRNTVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEVEEFSDGTIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 DEVEVEREESBOGSVL--GRWCGSGTVPGKOTSKGNHIRIRFVSDEYFPSEPGFCIHYSII- 163
                                                                                                                                                                                                                                                                                                                                                1 MLLIGLILLTSALAGQRIGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                                      2 DETIQVKGNGYVQSPRPPNSYPRNLLLTWRLHS-QENTRIQLVFDNQFGLEEAENDICRY
                                                                                                                                                                                                                                                                                             3; Gaps
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                                                                                                                                                                                                                              Query Match S8.3%; Score 1077.5; DB 1; Length 305; Best Local Similarity 75.7%; Pred. No. 1.5e-85; Matches 203; Conservative 27; Mismatches 35; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-876-813-56
Sequence 56, Application US/09876813
Sequence 56, Application US/09876813
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US/09/876,813
PRIOR PILING DATE: 2001-06-06
PRIOR PLING DATE: 2000-05-03
PRIOR FLING DATE: 2000-05-03
PRIOR PLING DATE: 1999-05-03
PRIOR PLING DATE: 1999-01-0
PRIOR PRIOR DATE: 1999-11-10
PRIOR PRIOR DATE: 1999-11-10
PRIOR PRIOR DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 --- LKBEVKLYSCTPRNFSVSIREELKR 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 EKNLKTNFYKYLAEGNFFNIIIVKLFKK 268
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: fusion polypeptide US-09-876-813-56
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ORGANISM: Artificial Sequence
                                                                                                                                                  ORGANISM: Homo sapiens
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        QY
        164 --MPQVTETT------SPSULPPSSLSLDLLNNAVTAFSTLEELIRYLEDD 206

        DD
        121 DFQPAAASETNWESVTSSISGVSYNSPSVTDP-TLIADALDKKIABFDTVEDLLKYFNPE 179

        QY
        207 RWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLALLKEEVKLYSCTPRNFSVSIREELKRT 266

        DD
        180 SWQEDLENWYLDTPRYRGRSY-HDRKSKVVDLALLTEEVKLYSCTPRNFSVSIREELKRT 238

        QY
        267 DTIFWPGCLLVKRCGGNCACCLHNCNBCQCVPRKYTKKYHBVLQLRPKTGVKGLHKSLTD 326

        DD
        239 DTIFWPGCLLVKRCGGNCACCLHNCNBCQCVPSKVTKKYHBVLQLRPKTGVRGLHKSLTD 298

        QY
        327 VALEHHBECDCVCRGNAGG 345

        DD
        299 VALEHHBECDCVCRGSTGG 317
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Search completed: November 25, 2003, 21:15:41 Job time: 14.6905 secs

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2003
```

using sw model OM protein - protein search, 2003, 20:59:34 ; Search time 14.7173 Seconds (without alignments) 2254.373 Million cell updates/sec November 25, ü

US-09-852-209A-7 1848 1 MLLIGLLLTSALAGQRTGT......DVALEHHEECDCVCRGNAGG 345 Perfect score:

Sequence:

0.5 BLOSUM62 Gapop 10.0 , Gapext Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d				
Result No.	Scor	g S	Lengt	DB	А	scriptio
	754	40.8	370	2	JC7592	spinal cord-derive
7	753	40.7	370		JC7591	spinal cord-derive
٣	191	10.3	707	7	JC2218	
4	190		823		A58788	procellagen C-endo
ហ	183.5		730		BMHU1	
9	183.5	0.0	927		JQ0948	A5 antigen precurs
7	181	9.8	986	٦	B58788	procollagen C-endo
œ	181	9.8	991		I49540	procellagen C-endo
Q	174.5	9.4	3623		T09456	
10	160	8.7	3623		T08618	
11	158	8.5	449	N	A55362	procollagen I C-pr
12	153	8.3	1057		A39288	ral
13	147.5		1524	~	130337	polyprotein - Afri
14	145.5	7.9	989	Н	A59271	Ra-reactive factor
15	144		669	1	154763	Ra-reactive factor
16	143.5	7.8	597	~	871352	Φ
17	141.5	7.7	1070		T31069	tolloid-BMP-1 like
18	140.5	7.6	3871	N	T22812	hypothetical prote
19	139	7.5	1594		T30549	bit
20	137.5	7.4	705	•	CIHURB	complement subcomp
21	135.5	7.3	1464	•	S58984	·
22	133.5	7.2	402	~	JH0403	procollagen I C-pr
23	128	6.9	277		A41735	hyaluronate-bindin
24	127		419	N	869207	vascular endotheli
25	126.5		579	2	JC7629	membrane-type friz
26	125.5		245	-1	TVCTSS	platelet-derived q
27	125.5		167	~1	T30018	hypothetical prote
28	123	6.7	275	~	JC6506	tumor necrosis fac
53	122.5		2403	~	A59386	sanko - human

338 FKRRGKAKNAALVDIQLDHHERCDCIC 364

g

CRP-ductin-alpha   TSG-6 homolog PS4	ebnerin precursor	platelet-derived g	platelet-derived g	platelet-derived g	complement subcomp	platelet-derived g	PDGF-related trans	complement subcomp	16K vascular endot	hypothetical prote	UVS.2 protein - Af	platelet-derived g	platelet-derived g	platelet-derived g
T42721 A47290	A57190	I51551	808220	I51550	505008	PFHUG2	TVMVSS	JC6554	D49530	T33161	151569	S25097	B28964	PFHUG1
00	0	N	7	N	ч	н	Н	~	N	~	~	7	~	н
2083	1290	200	215	226	695	241	226	694	148	321	319	225	196	211
70 4	4.	6.2	6.2	6.2	6.1	6.1	0.9	5.9	5.9	5.8	5.6	5.6	5.6	5.6
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119.5 6.	117.5	114.5	114.5	114.5	113	112.5	111.5	109	108.5	107	104	103.5	103	103

## ALIGNMENTS

```
Claccesion: UC7592
R.Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
R.Hamada, T.; Ui-Tei, K.; Imaki, J.; Miyata, Y.
B.Jochem. Biophys. Res. Commun. 280, 733-737, 201
A.Fitle: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGF-C
A.Reference number: UC7591; MUID:21092670; PMID:11162582
A.Contents: Fetal brain
A.Accession: UC7592
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-370 c-HAM>
A.Molecule type: mRNA
A.Residues: 1-370 c-HAM>
A.Gone: Scdgf-B
F;1-17/Domain: Secretory signal sequence #status predicted cSIG>
F;1-17/Domain: Secretory signal growth factor-B #status predicted cMAT>
F;22-170/Region: CUB domain #status predicted
F;22-370/Region: CuB domain #status predicted
F;23-370/Region: Cub and motif #status predicted
F;294-308/Region: conserved motif #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 ESNHLTDLYRRDENIRVIGTGHVQSPRFPNSYPRNLLLTWRLHS-QEKTRIQLAFDHQFG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 LEDPEDDICKYDFVEVEREPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 PGFCIHYSII---MPQ-----VTET-----TSPSVLPPSSLSLDLLNNAVTAFST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 SVNLREBLKLTNAVFFPRCLLVQRCGGNCGCGTLNWKSCTCSSGKTVKKYHEVLKFEFFGH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 LEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 SVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP-- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
spinal cord-derived growth factor-B precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 EQNGVQD-PRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.8%; Score 754; DB 2; Length 37 ilarity 46.2%; Pred. No. 1.4e-55; Conservative 62; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KTGVKGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 151; Conserv
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55 NGSIHSPKRPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
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A;Cross-references: GDB:125203; OMIM:112264
A;Map position: 8p21-8p21
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Best Local Similarity
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NyAlternate names: bone morphogenic protein 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999
C;Accession: JC2218
C;Accession: JC2218
R;Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
Gene 134, 257-261, 1993
A;Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prote
A;Reference number: JC2218; MUID:94085787; PMID:8262384
A;Accession: JC2218
A;Molecule type: mRNA
A;Residues: 1-707 <AME>
A;Cross-references: GB:L12249; NID:9406540; FIDN:AAA16313.1; PID:9406541
C;Comment: This protein induces ectopic cartilage formation in vivo.
C;Superfamily: procollagen C-endopeptidase; astacin homology; CIr/Cis repeat homology; C;Cypuerfamily: astacin homology astacin homology complement Ir/Is-like repeat
F;285-394/Domain: CIr/Cis repeat homology CIRI>
F;285-394/Domain: CIr/Cis repeat homology CIRI>
F;398-510/Region: complement Ir/Is-like repeat
Spinal cord-derived growth factor-B precursor - human c)Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Species: Homo sapiens (man) Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal Spinal 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 LEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 SVNIREELKLANVVFFPRCLLVQRCGGNCGCGTVNWRSCTCNSGKTVKKYHBVLQFBPGH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGFCIHYSII---MPQVTETT------SPSVLPPSSLSLDLINNAVTARST 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 SVSIRBELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP-- 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 LEDPEDDICKYDFVEVEEPSDGSVL - GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 EQNGVQD-PRHERVVTISGNGSIHSPKPPHTYPRNMVLVWRLVAVDENVRIQLTFDERFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.7%; Score 753; DB 2; Local Similarity 45.3%; Pred. No. 1.7e-55; les 148; Conservative 59; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 -KTGVKGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    338 IKRRGRAKTMALVDIQLDHHERCDCIC 364
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A;Accession: A37278
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kosidues: 1-702, 'EKRPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A;Cross-treferences: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
G. Biol. Chem. 269, 32572-32578, 1994
A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encomplemence number: A58788; MUID:95096114; PMID:7798260
A;Accession: A58788
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F;398-507/Domain: CIr/CIs repeat homology <CIR2>
F;554-566/Region: GGF homology <EGF>
F;554-666/Region: complement Ir/Is-like repeat
F;554-667/Domain: CIr/Cis repeat homology <CIR3>
F;62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;176,105,295,325/Binding site: zinc (His, His, His, Tyr) #status predicted
F;177/Active site: dlu #status predicted
F;528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                        55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form HIS - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: A37278; A58788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities. A;Title: Novel mumber: A37278; MUID:89072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N,Alternate names: bone morphogenic protein splice form BMP-1/His
C;Species: Homo sapiens (man)
C;Date: 28-Mar.1998 #sequence_revision 09-Apr-1998 #text_change 18-Jun-1999
C;Accession: A37278; A58788
                                                                                                                                                                                                                                                                                                                                                                                                                                                     562 NGSINSPGWPKEYPPNKNCIWQLVAPTQ-YRISLKFDQ---PETBGNDVCKYDFVEVRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 703-823 <TAX>
A;Cross-references: GB:L35278; NID:g619423; PIDN:AAC41703.1; PID:g619424
C;Genetics:
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F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status
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                                                                                                                                                                                                                                                                          Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Indels
                                                                                                                                                                                                                                                                          Query Match 10.3%; Score 191; DB 2; Best Local Similarity 45.2%; Pred. No. 6.7e-08; Matches 47; Conservative 16; Mismatches 33;
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A; Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen typic; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cis repeat homology; C; Superfamily: procollagen C-endopeptidase; astacin homology; C; Exywords: alternative splicing; bera-hydroxyasparagine; bone; calcium; duplication; G; P; 1-22, Domain: signal sequence #status predicted <SIG.
F; 21-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predicted F; 130-321/Domain: astacin homology <CIRI>
F; 322-431/Domain: Clr/Cis repeat homology <CIRI>
F; 435-544/Domain: Clr/Cis repeat homology <CIRI>
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A;Residues: 1-70.2, EKKPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
R;Takahara, K.; Lyons, G.E.; Greenspan, D.S.
C. Biol. Chem. 269, 32572-32578, 1994
A;Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoral parence number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He
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C;Date: 28-Mar-1998 #sequence_revision 09-Apr-1998 #text_change 16-Jul-1999
C;Accession: A37278; BS9788
S;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; He Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 VTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 EVIDGDNANGQLLGKYCGK-IAPSPLVSTGPSIFIRFVSDYETPG-AGFSIRYEVFKTGP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 ECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFA---PKNOEIV--LEFESFELEADS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 IKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHYQRIMINFNPHFDLEDRE---CKYDYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 QVTE--TTSPSVLP-----PSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDS
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A;Residues: 703-986 <TAK>
A;Cross-references: GB:L35279; NID:g619860; PIDN:AAC41710.1; PID:g619861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 927;
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A, Reference number: JH0466; MUID: 91337458; PMID: 1908252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.9%; Score 183.5; DB 1
30.7%; Pred. No. 4.1e-07;
tive 34; Mismatches 65
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A,Cross-references: GDB:125203; OMIM:112264
A,Map position: 8p21-8p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.7%;
Matches 55; Conservative
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F;13-730/Product: procollagen C-endopeptidase splice form BMP1 #status predicted <MAT>
F;130-231/Domain: astacin homology <ASIC>
F;131-0321/Domain: clr/Cls repeat homology <CIRI>
F;51-544/Domain: Clr/Cls repeat homology <CIRI>
F;551-84/Domain: Clr/Cls repeat homology <CIRI>
F;551-867/Domain: Clr/Cls repeat homology <CIRI>
F;51-1700/Domain: Clr/Cls repeat homology <CIRI>
F;51-1700/Domain: Clr/Cls repeat homology <CIRI>
F;51-1700/Domain: Clr/Cls repeat homology <CIRI>
F;51-1700/Domain: Clr/Cls repeat homology <CIRI>
F;51-170,132,323,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163-319,182-323,273/Binding site: carbohydrate (Asn) #status predicted
F;121,44/Active site: Glu #status predicted
F;255/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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A5 antigen precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: Senopus laevis (African clawed frog)
C; Accession: UH0466; JQ0948
R; Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A; Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A37278; E58788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730; PMID:3201241
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                                                                                                                                                                                                                                                                                                                                                                                                                                  procollagen C-endopeptidase (EC 3.4.24.19) precursor, splice form BMP1 - human NiAlternate names: borne morphogenic protein 1 (BMP1) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEE- 113
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NGSITSPGWPKEYPPNKNCIWQLVAPTQ-YRISLQFD---FFETEGNDVCKYDFVEVRSG 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44; Indels 15; Gaps
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A;Residues: 1-730 <WOZ>
A;Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
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                                                               114 -PSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY-
                                                                                                                                                                                                                                       13 HLSGLELLLCPHALVDTVPA--PPSALHGD 740
                                                                                                                                                                                                 -----SIIMPQVTETTSPSVLPPSSLSLD 184
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nes 49; Conserv
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A; Reference number: Z16677; MUID: 98241400; PMID: 9572993
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                                          A; Accession: T09456
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                                                                                                                   F;747-856/Domain: CIr/CIS repeat homology <CIR4>
F;747-856/Domain: CIr/CIS repeat homology <CIR5>
F;860-973/Domain: CIr/CIS repeat homology <CIR5>
F;91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;91,142,332,363,529/Binding site: carbohydrate (Asn-563,559-572,574-587,591-617,644-66
F;213,217,223,272/Binding site: zinc (His, His, His, His, Tyr) #status predicted
F;214,Active site: Glu #status predicted
F;565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
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C,Species: Homo sapiens (man)
C,Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
C,Accession: T09456
K,Rozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup, N
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular characteriz
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Dev. Biol. 163, 175-183, 1954
A.Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is A;Reference number: 149540; MUID:94229342; PMID:8174772
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C.Species: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
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A;Residues: 1-991 <RES>
A;Cross-references: GB:L24755; NID:g439606; PIDN:AAA37306.1; PID:g439607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 986;
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42.6%; Pred. No. 7.2e-07;
rative 16; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.8%; Score 181; DB 1; Best Local Similarity 42.6%; Pred. No. 7.1e-07; Matches 46; Conservative 16; Mismatches 38;
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EGF homology <EG2>
            homology
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Best Local Similarity
Matches 46; Conserv
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            F;551-587/Domain: E;591-700/Domain: C
F;707-742/Domain: E;747-856/Domain: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membrane F;1-20/Domain: signal sequence #status predicted <SIG> $213.9523/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT> F;133-164/Domain: BGF homology <BGF1> F;436-467/Domain: BGF homology <BGF2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intrinsic factor-B12 receptor CUBILIN precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
C;Accession: T08618
R;Mosetrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault, J. Boll. Chem. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin B12 receptor and target of teratogenic antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1031 AHE-GFSINYEAIDASSVCLYDYTDNFGMLSSPN-FPNNYPSNWECIYRITVGLNQQIAL 1088
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                                                                        A;Residues: 17-3623 <KOZ>
A;Residues: 1-3623 <KOZ>
A;Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AACG2612.1; PID:g3929529
C;Genetics:
A;Map position: 10p12
C;Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
C;Keywords: receptor; vitamin B12 uptake
F):24/Domain: signal sequence #status predicted <SIG>
F):24/Domain: Egralus factor-B12 receptor #status predicted <MAT>
F;25-3623/Product: intrinsic factor-B12 receptor #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2173 GHFCGSHASSTLFTSDNOMFVQFISDHSNEGOGFKIKYEAKSLACGGNVYIHDADSAGYV 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-3623 <MOE>
A;Cross-references: EMBL:AF022247; NID:g3834379; PIDN:AAC71661.1; PID:g3834380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 DERFGLEDPEDDICKYDFVEVEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYF 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 PSEPGFCIHY-----SIIMPQVTET----TSPSVLP---PSS-----LSLDLLNNAVT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AFS--TLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEEVKLY- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 QLSSDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      924 KPSSDKLECG-----EVLTAS-TGIIESPGHPNVYPRGVNCTWHVV-VQRGQLIRLEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 -SPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 GORTGTRAESNLSSK----LQLSSD--KEONGVODPRHERVVTISGNGSIH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.4%; Score 174.5; DB 2; Length 3623; 31.9%; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: intrinsic factor-B12 receptor cubilin; EGF homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2290 APILSKFCGT-SIPSSQWSSGEVMYLRFRSDN-SPTHVGFKAKYSI 2333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 GSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 160; DB 2; Length 36
86.8%; Pred. No. 0.00022;
Ve 44; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: Z16459; MUID:98148073; PMID:9478979
A;Accession: T08618
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26; Mismatches
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C;Accession: T30337
R;Yang, J.C.; Lindsay, L.L.; Hedrick, J.L.
submitted to the EMBL Data Library, March 1998
A;Description: cDNA cloning of ovochymase, a chymotrypsin-like protease released from >
A;Reference number: Z20829
                       astacin homology; Clr/Cls ref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ra-reactive factor (BC 3.4.21.-) 2 precursor - human N_t Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 SDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQ-----VT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETTSPSVLPPSSLSLDLLINNA-VTAFSTLEELIRYLEPD----RWQVDL-----DS 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: markA
A;Residues: 1-1524 <7AN>
A;Residues: T-1524 <7BN: WBL:US1290; NID:G2981640; PID:G2981641; PIDN:AAC24717.1
                                                                                                                                                                                                                                                                                                           Tyr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Feb-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LAGORIGIRAESNLSSKLOLSSDKEQNGVQDPRHERV----VTISGNGSIHSPKFPHTYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 RNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE--PSDGSVLGRWCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV-EEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
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                                                                                                                                                                                                                                                                                                                                                                                           Length 1057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                    C, Superfamily: dorsal-ventral patterning protein tolloid; as C, Keywords: duplication; hydrolase; metalloproteinase; zinc F;136-239/Domain: astacin homology <AST>
F;352-464/Domain: CIr/CIs repeat homology <CIR1>
F;468-578/Domain: CIr/CIs repeat homology <CIR2>
F;585-620/Domain: GIr/CIs repeat homology <CIR2>
F;585-4740/Domain: GIr/CIs repeat homology <CIR3>
F;747-782/Domain: GIF/CIs repeat homology <CIR3>
F;747-782/Domain: GIF homology <GG2>
F;787-896/Domain: CIr/CIs repeat homology <CIR4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: tryosin related polyprotein; trypsin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                           F;900-1013/Domain: Clr/Cls repeat homology <C1R5>
F;221,225,231,280/Binding site: zinc (His, His, His, F;222/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                           8.3%; Score 153; DB 1;
illarity 33.3%; Pred. No. 0.00018;
Conservative 28; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.0%; Score 147.5; DB 2
28.7%; Pred. No. 0.00082;
tive 34; Mismatches 73
Cross-references: FlyBase: FBgn0003719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 KLPPNIKT-RSNOMYIRFVSD 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       127 GTVPGKQTSKGNHIRIRFVSD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyprotein - African clawed frog
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Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T30337
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Accession: A33288
R; Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
R; Shimell, M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B.
A; Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bone A; Reference number: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
A; Accession: A39288
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R;Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show
A; Biol. Chem. 269, 26280-26285, 1994
A;Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, p
A;Reference number: A55362; MUID:95014462; PMID:7523404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
1089 HFTDFTLEDYFGSQCVDFVEI-RDGGYE-TSPLVG---1Y--CGSVLPPTIISHSNKLWL 1141
                                                                                                         -----YWDGS--STGCGGN----LTTPTGVLTSPNYPM 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281
                                                       ----SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVT 302
                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDERFGLEDFEDDICKYDFVEV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:L33799; NID:g642907; PIDN:AAA61949.1; PID:g642908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;37-146/Domain: CIr/Cis repeat homology <C1R1>
F;159-270/Domain: CIr/Cis repeat homology <CIR2>
F;26/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form)
F;26/Modified site: pyrrolidone carboxylic acid (Gln) (she predicted F;26,431/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:305468; OMIM:600270
A;Map position: 7q21.3-7q22
C;Superfamily: CIT/CIS repeat homology
C;Keywords: extracellular protein; glycoprotein; pyroglutamic acid
F;1-25/Domain: signal sequence #status predicted <SIG>F;26-449/Product: #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%; Score 158; DB 2; Length 449; 34.5%; Pred. No. 2.2e-05; tive 21; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                   procollagen I C-proteinase enhancer protein precursor - human
                                                                                                                                                                                                                         1184 PYYHSSECYWRLEASHG-SPFELEFODFHLEHHPSC 1218
                                                                                                                                                                 303 KKYHE---VLQLRPKTGVKGLHKSLTDVALEHHEEC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Status: not compared with conceptual translation A;Molecule type: mRNA
A;Residues: 1-449 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PQVTETTSPSV-LPPSS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OGPGPKRGTEPKVKLPPKS 300
                                                                                        : | : | |
1142 KFKSDAALTAKGFSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB: PCOLCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
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7;

18; Gaps

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A,Gener GDB:MASP1, GDB:CRARF; CRARF1, PRSS5, MASP
A,Cross-references: GDB:361104; GDB:330954; OMIM:600521
A,Map position: 3427-3448
A,Cross-references: GDB:361104; GDB:330954; OMIM:600521
A,Map position: 3427-3448
C,Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement factor
C,Keywords: beta-hydroxyasparagine; complement pathway; duplication; glycoprotein; hydr
F;1-17/Domain: sland sequence #stetus predicted <SIG>
F;18-448,449-699/Product: Ra-reactive factor #status predicted <MAT>
F;19-135/Domain: Clr/Cls repeat homology <CIR1>
F;18-294/Domain: Clr/Cls repeat homology <CIR2>
F;18-294/Domain: complement factor H repeat homology <FH1>
F;301-362/Domain: complement factor H repeat homology <FH2>
F;449-691/Domain: trypsin homology <IRV>
F;449-691/Domain: trypsin homology <IRV>
F;449-1184-149-115-153-166,168-181,185-212-2260,301-349,329-362,367-414,397-432,436-572
F;159/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;448-449/Cleavage site: His, Asp, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 GSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEPS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 DGSVLGRWCGSGTVPGKQT----SKGNHIRIRFVSDEYFPSE--PGFCIHYSII 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDQVLATFCGRETTDTEQTPGQEVVLSPGSFMSITFRSD--FSNEERFTGFDAHYMAV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 GQIQSPGYPBSYPSDSEVTWN-ITVPDGFRIKLYF-MHFNLE--SSYLCEYDYKVE--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.8%; Score 144; DB 1; Length 699; 34.7%; Pred. No. 0.00059; tive 19; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: November 25, 2003, 21:05:30 Job time: 15.7173 secs
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Best Local Similarity 34.7%
Matches 41; Conservative
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A; Experimental cycles (JEB)
A; Experimental source: 1.686 (JEB)
A; Experimental source: 1.686 (JEB)
A; Cross-references: GB: Y09256; NID: g4007626; PIDN: CAA71059.1; PID: g4007627
A; Note: submitted to GenBank, December 1996
A; Note: parts of this sequence, including the amino end of the mature protein, were dete C; Genetics:
A; Genetics:
A; Genetics: GBB: 6071500
A; Note: parts of this sequence, including the amino end of the mature protein, were dete C; Genetics: references: GDB: 6071500
A; Cross-references: GDB: 6071500
A; Map position: 1936.2-1p36.3
C; Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement pathway; duplication; hydrolase; serine F; C; Superfamily: complement saraus predicted <SIGS product: Ra-reactive factor 2 #status predicted <MAT>
F; 19-134/Domain: Clr/Cls repeat homology <CIR1>
F; 142-180/Domain: Clr/Cls repeat homology <CIR2>
F; 166-130/Domain: complement factor H repeat homology <FH1>
F; 166-130/Domain: complement factor H repeat homology <FH2>
F; 166-130/Domain: complement factor H repeat homology <FH2>
F; 166-130/Domain: complement factor H repeat homology <FH2>
F; 166-130/Domain: complement factor H repeat homology <FH3>
F; 166-130/Domain: complement factor H repeat homology <FH3>
F; 166-130/Domain: complement factor H repeat homology <FH3>
F; 166-130/Domain: complement factor H repeat homology <FH3>
F; 166-130/Domain: complement factor H repeat homology <FH3>
F; 1672-90, 142-156, 165-1160, 184-211, 241-259, 300-348, 328-361, 366-412, 396-430, 434-552, F; 444-445/Claevage site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F; 444-445/Claevage site: His, Asp, Ser #status predicted
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A, Residues: 1-699 <SAT>
A, Residues: 1-699 <SAT>
A, Cross-references: GB-2593; NID:g790963; PIDN:BAA05928.1; PID:g471128
R, Takada, F.; Takayama, Y.; Hatsuse, H.; Kawakami, M.
Biochem. Biophys. Res. Commun. 196, 1003-1009, 1993
A, Title: A new member of the Cls family of complement proteins found in a bactericidal
A, Reference number: JN0883; MUID:94059062; PMID:8240317
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
C;Accession: A:9271
R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, M
Nature 386, So6-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates
A;Reference number: A:99271; MUID:97242412; PMID:9087411
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A;Cross-references: DDBJ:D17525; NID:g439712; PIDN:BAA04477.1; PID:g439713
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                          A,Accession: A59271
A,Status: nucleic acid sequence not shown; not compared with conceptual translation
A,Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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N'Alternate names: mannose binding protein-associated serine proteinase 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 SDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYS 161
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Matches 33; Conserv
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A; Status: prelimina
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us-09-852-209a-7.rsp

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HSSP; P00736; 1APQ.
MEROPS; M12.005; -.
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P98070:
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1896.117 Million cell updates/sec
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                                                              November 25, 2003, 20:55:48 ; Search time 8.55655 Seconds
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014786
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                          Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                     127863 seqs, 47026705 residues
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NRP2_MOUSE
VEGD_RAT
TLD_DROME
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NRP1_HUMAN
TLD_BRARE
NRP1_RAT
NRP1_MOUSE
NRP1_CHICK
SPAN_STRPU
SPAN_STRPU
PCO1_HUMAN
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MAS2 HUMAN
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VEGD HUMAN
VEGD MOUSE
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TSG6 HUMAN
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PDGA_XENLA
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P15156 mesocricetu P01127 homo sapien	P26617 cavia porce P01128 simian sarc Q9y5y6 homo sapien	P52585 orf virus ( P49765 homo sapien	Q9x849 bos taurus Q05028 rattus norv	Q95229 ovis aries P04085 homo sapien
CASP_MESAU PDGB_HUMAN	VEGA_CAVPO TSIS_SMSAV ST14_HUMAN	VEGH_ORFN7 VEGB_HUMAN	UVSZ AENLA VEGB_BOVIN PDGB_RAT	PDGB_SHEEP PDGA_HUMAN
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113	111.5 111.5 109	108.5	103.5 103.5	103.5
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## ALIGNMENTS

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les 55; Conserv
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MEDLINE=3137458; PubMed=1908252;
MEDLINE=3137458; PubMed=1908252;
Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
Takagi S., Hirata T., Agata K., Mochii M., Eguchi G., Fujisawa H.;
Takagi S., Hirata T., Agata K., Mochie and coagulation molecule,
The As antigen, a candidate for the neuronal recognition molecule,
The As antigen, a candidate for the neuronal recognition factors.";
The As antigen, a candidate for the neuronal recognition of the Neuron 7:255-307(1991)
The As antigen, a candidate for the neuronal recognition of the Neuron 7:255-307(1991)
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PROSITE; PS00101, ASX. HYDROXYL; 1.
PROSITE; PS00022; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
Growth factor; Cytckine; Repeat; Bone; Cartilage; Hydrolase; Protease; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
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28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2011in-1 precursor (As protein) (As antigen).
Xenopus laevis (African clawed frog).
Bukaryota; Metazca; Chordaca; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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BY SIMILARITY.
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(BY SIMILARITY)
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01-DEC-1992 (Rel. 24, Last seq
28-FEB-2003 (Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 VIISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 EVIDGDNANGQLLGKYCGK-IAPSPLVSTGPSIFIRFVSDXETPG-AGFSIRXEVFKTGP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QVTE--TTSPSVLP-----PSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50060; MAM-2; 1.
Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 PROBABLE.
424 BY SIMILARITY.
584 BY SIMILARITY.
150 N-LINKED (GLCNAC. . . ) (POTEN
261 N-LINKED (GLCNAC. . . ) (POTEN
300 N-LINKED (GLCNAC. . . ) (POTEN
523 N-LINKED (GLCNAC. . . ) (POTEN
844 N-LINKED (GLCNAC. . . ) (POTEN
103416 MW; AF6B323B0A4C789D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 183.5; DB 1;
30.7%; Pred. No. 4e-07;
tive 34; Mismatches 65;
-i- SIMILARITY: BELONGS TO THE NEUROPLIN FAMILY.
-i- SIMILARITY: Contains 2 CDB domains.
-i- SIMILARITY: Contains 2 F5/8 type C domains.
-i- SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUB 2.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE.
PROBABLE.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000899; CUB domain.
InterPro; IPR000899; CUB domain.
InterPro; IPR000899; MAM domain.
Iffam; PP00411; CUB; 2.
Pfam; PP00641; CUB; 2.
Pfam; PP00629; MAM; 1.
PRINTS; PR00020; MAMDONAIN.
SMART; SM00042; CUB; 2.
SMART; SM0031; FASBC; 2.
SMART; SM0031; FASBC; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01286; FASBC; 2.
PROSITE; PS01286; FASBC; 3.
PROSITE; PS01286; FASBC; 3; 2.
PROSITE; PS00740; MAM; 1.
PROSITE; PS00740; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUB 1
                                                                                                                                                                                                                                                                                                                                                                        EMBL; D10467; BAA01260.1; -. HSSP; P12259; 1CZT.
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POTENTIAL
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EMBL, W22488; AAA5183.1; --
EMBL, Y08723; CAA69973.1; --
EMBL, Y08725; CAA69975.1; --
EMBL, Y08725; CAA69975.1; --
EMBL, L35278; AAC41703.1; --
EMBL, L35278; AAC41703.1; --
EMBL, L35278; AAC41710.1; --
FIR, A37278; B58788.
HSSP; P00736; 1APQ.
MEROPS; M12.005; --
Genew; HGNC:1067; BMP1.
                                                                     Name=BMP1-6;
 Name=BMP1-4;
                                                                                                        Name=BMP1-7;
                                 Name=BMP1-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
ACT_SITE
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DOMAIN
DOMAIN
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DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
MEDLINE-98160316; PubMed-9500680;
Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
"Three alternatively spliced variants of the gene coding for the human
bone morphogenetic protein-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Takahara K., Lyons G.E., Greenspan D.S., "Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are encoded by alternatively spliced transcripts which are differentially expressed in some tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21336528; PubMed=11283002;
Garrigue-Anter L., Barker C., Kadler K.E.;
Garrigue-Anter L. antho acid residues in bone morphogenetic
protein-1 important for procollagen C-proteinase activity.";
J. Biol. Chem. 276:26237-26242(2001).
-! FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II
AND II. INDUCES CARTILAGE AND BONE FORMATION.
-!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at
Ala-|-Asp in type I and II procollagens and at Arg-|-Asp in type
                                                                                                                                                                                                                                                                                                                                                                                        is identical to the protein previously identified as bone morphogenic
                                                                                                                                                                                                                                                                                                                                                                       "The C-proteinase that processes procollagens to fibrillar collagens
                                                BMP1 HUMAN STANDARD; PRT; 986 AA.
P13497; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: Binds 1 zinc ion per subunit (By similarity).
ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDOPEPTIDASE ENHANCER PROTEIN.
                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A.; "Novel regulators of bone formation: molecular clones and
                                                                                                                                                                                                                                                                                                                                     Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V., Prockop D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=7;
Name=BMP1-3;
                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P13497-7; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFIDE BOND IN METALLOPROTEASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=P13497-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 269:32572-32578(1994).
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM BMP1-3). TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM BMP1-1).
MEDLINE=89072730; PubMed=3201241;
                                                                                                                                                                                                                                                                                                                      MEDLINE=96209868; PubMed=8643539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=95096114; PubMed=7798260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Med. 76:141-146(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 242:1528-1534 (1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=BMP1-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=BMP1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activities."
                                                                                                                                                                                                                                                                                                                                                                                                                    protein-1
                  RESULT 3
BMP1_HUMAN
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BGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
CUB 4.
CUB 5.
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R SMART; SMO012; CUB; S.

R SMART; SMO0179; EGF_CA; 2.

R SMART; SMO0179; EGF_CA; 2.

R SMART; SMO0179; EGF_CA; 2.

R PROSITE; PS00142; ZIMC; 1.

R PROSITE; PS001180; CUB; 5.

R PROSITE; PS00122; EGF_1; PALSE_NEG.

R PROSITE; PS01186; EGF_2; 2.

R PROSITE; PS01187; EGF_CA; 2.

R Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Metalloprotease; EGF-like domain; Zinc; Calcium; Signal; Glycoprotein; Zymogen; Alternative Splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BONE MORPHOGENETIC PROTEIN 1 METALLOPROTEASE.
IsoId=P13497-3; Sequence=VSP_005463, VSP_005464;
                                                                   Isold=P13497-4; Sequence=VSP_005465, VSP_005466;
                                                                                                                                                                                                          Isold=P13497-6; Sequence=VSP_005469, VSP_005470;
-! TISSUB SPECIFICITY: Ubiquitous
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
-!- SIMILARITY: Contains 2 BGF-like domains.
-!- SIMILARITY: Contains 5 CUB domains.
                                                                                                                                          IsoId=P13497-5; Sequence=VSP_005467, VSP_005468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 11264; ---
GO; GO: GOODS576; C: extracellular; NAS.
GO; GO: O008576; C: extracellular; NAS.
GO; GO: O008576; C: extracellular; NAS.
GO; GO: O001502; P: cartilage condensation; TAS.
GO; GO: O007275; P: development; TAS.
InterPro; IPRO01505; Astadin.
InterPro; IPRO01891; EGF Ca.
InterPro; IPRO01891; EGF Ca.
InterPro; IPRO06209; EGF like.
InterPro; IPRO06209; EGF like.
InterPro; IPRO06205; Zn. WTpeptdse.
Pfam; PF01400; Astadin; 1.
Pfam; PF01400; Astadin; 1.
Pfam; PF00189; EGF; 2.
PRINTS; PR00480; ASTACIN.
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EAGCDHKVTSTSGTITSPNWPDKYPSKKECTWAISSTPGHR
VALTPRMENISSPERGAYDHLEVPDRDAKAFVLGRFCG
-> VLEGAGDRHSHLSGLELLICHALVOTYPAPPSAHGD
THAHTHTHTHTPLALCPIAQETCRGPPLGASRLSPQGPGHLTLA
                                                                                                                                                                                                                                                                                                                                                               DKDECSKDNGGCQQDCVNTFGSYECQCR -> EKRPALQPP
RGRPHQLKFRVQKRNRTPQ (in isoform BMP1-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVPKYEVNGVKPPIGQR -> VLHSSLLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQEGSYLDFWDTHRGDPKPRRRRKSLKTFSLTPATFRGIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEYNFLKMEPQEVESLGETYDFDSIMHYARNTFSRGIFLDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> GC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 NGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKDECSKDNGGCQQD -> GGELFGLLGHPPRRP (in
                                                                                                                                                                                                                                                                  D (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGGFLTKLNGSITSPGWPKEYPPNKNCIWQLV
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 986;
                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP_005461.
Missing (in isoform BMP1-1).
/FTId=VSP_005462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (in isoform BMP1-4).
/FTId=VSP 005463.
dissing (in isoform BMP1-4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP 005465.
Missing (In isoform BMP1-5).
/FTId=VSP_005466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId=VSP_005467.
Missing (in isoform BMP1-6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (in isoform BMP1-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.8%; Score 181; DB 1;
42.6%; Pred. No. 6.8e-07;
trive 16; Mismatches 38,
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15-SEP-2003 (Rel. 42, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE-98188039; PubMed-9529250;
Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
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(BY SIMILARITY)
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SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=97433084; PubMed=9288753;
He Z., Tessier-Lavigne M.;
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014786; 060461;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO; GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS. GO; GO:0007411; P:axon guidance; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                   binding to KDR
                                                                                                                                                                                                                    Soker S., Klagsbrun M.; "Identification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor
                                                                                                      Gagnon M.L., Bielenberg D.R., Gechtman Z., Miao H.-Q., Takashima S.,
"Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to inhibit its binding to cells. It may also induce apoptosis by sequestering VEGF-165. May bind as well various members of the semaphorin family. Its expression has an averse effect on blood vessel number and integrity.
                                                                                                                                                                                                                                                                                                                                                                    outside the nervous system. It mediates the chemorepulsant activity of semaphorins. It binds to semaphorin 3A, The PLGF-2 isoform of PGF and VEGF-B. Coexpression with MDR results in increased VEGF-165 binding to as well as increased chemotaxis. It may regulate VEGF-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                           SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY. SIMILARITY: Contains 2 CUB domains. MINILARITY: Contains 2 F5/8 type C domains. SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000)
                                                                         TISSUE=Prostatic adenocarcinoma;
MEDLINE=20183929; PubMed=10688880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF018956; AAC51759.1; -.
EMBL; AF016050; AAC12921.1; -.
EMBL; AF145712; AAF44344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:8004; NRP1.
MIM; 602069; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              angiogenesis.
                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted
                                                                                                                                                                 activity
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50 VIISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                  110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYPPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                              145
                                                                                                                                                                                                                                                                                                                                                                     87
88 EVFDGENENGHFRGKFCGK-IAPPPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGP
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          166 QVTE--TTSPSVLP-----PSSLSLDLLNNAVTAFSTLEELIRY----LEPD 206
                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                               / Match 9.5%; Score 176; DB 1; Length 923; Local Similarity 32.6%; Pred. No. 1.6e-06; No. 57; Conservative 24; Mismatches 68; Indels 33;
                                                                                                                                                                                                                                                                        EFP -> GIK (in isoform 2).
/FTId=VSP 004339.
/FIId=VSP 004340.
K -> E (IN REF. 1).
E -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                   103120 MW; ADEADC4A849E5D57 CRC64;
                                                                                                                                             NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                             BY SIMILARITY.

N-LINKED (GLONAC. .) (;

N-LINKED (GLONAC. .) (;

N-LINKED (GLONAC. .) (;

N-LINKED (GLONAC. .) (;

N-LINKED (GLONAC. .) (;

N-LINKED (GLONAC. .) (;
                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                   F5/8 TYPE C
F5/8 TYPE C
                                                                                                                                                                                                                  PROBABLE. PROBABLE.
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749
855
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923 AA;
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1022 AA

STANDARD;

TLD BRARE 057460;

TLD BRARE ID TLD BI AC 057460 RESULT 6

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PROMO48; ASTACIN.
SMART; SM001042; CUB; 5.
SMART; SM00104; EGF_CA; 2.
SMART; SM00104; EGF_CA; 2.
PROSITE; PS00010; ASX_HYDROXYL; 2.
PROSITE; PS00022; EGF_1; FALSE_NEG.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS01148; EGF_2; 2.
PROSITE; PS01142; ZINC_PROTEASE; 1.
PROSITE; PS01142; ZINC_PROTEASE; 1.
Developmental protein; Hydrolase; Protease; Metalloprotease; Zinc; Metal-binding; Calcium; EGF-like domain; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99307076; PubMed=10375503;
Connors S.A., Trout J., Ekker M., Mullins M.C.;
"The role of tolloid/mini fin in dorsoventral pattern formation of the
zebzafish embryo.";
Development 126:3119-3130(1999).
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amontation update)
Dorsal-ventral patterning tolloid protein precursor (BC 3.4.24.-)
(Mini fin protein).

(Mini fin protein).

Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio repio (Zebrafish) (Panio rerio).

Cyprinidae, Danio.
                                                                                                                                                                                                                               Blader P., Ragtegar S., Fischer N., Straehle U.; "Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid."; Science 278:1937-1940(1997).
                                                                                                                                                                                   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZETM; ZDB-GENE-990415-265; tolloid.
InterPro; IPR00156; Astacin.
InterPro; IPR00155; Ast Mydroxyl.
InterPro; IPR001689; CUB domain.
InterPro; IPR001881; EGF Ca.
InterPro; IPR002081; EGF Ta.
InterPro; IPR006205; EGF Tike.
InterPro; IPR006025; Zn MTpeptdse.
InterPro; IPR006025; Zn MTpeptdse.
InterPro; IPR006025; Zn MTpeptdse.
Ffam; PF00401; CUB; 5.
Pfam; PF00008; EGF; 2.
                                                                                                                                                                                                   TISSUE-Gastrula;
MEDLINE-98057457; PubMed-9395394;
                                                                                                                                                                                                                                                                                                FUNCTION, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF027596; AAC60304.1; -. HSSP; P35555; 1EMN.
MEROPS; M12.016; -.
                                                                                                                                    Cyprinidae; Dani
NCBI_TaxID=7955;
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DOMAIN METAL

METAL

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OMAIN COMAIN

DOMAIN DOMAIN

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Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,

"Ginty D.D.;
"Interceptor.";
"Cell 90:753-762(1997).
"Cell 90:753-762(1997).
"Cell 90:753-762(1997).
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N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
N-LINKED (GLCNAC. ) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL. CYTOPLASMIC (POTENTIAL)
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31.5%; Pred. No. 3.4e-06;
tive 21; Mismatches 67,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F5/8 TYPE C 1.
F5/8 TYPE C 2.
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InterPro; IPR000421; FAS® C.
InterPro; IPR000998; MAM Gomain.
Pfam; PP00431, CUB; 2.
Pfam; PP00424; FS_F8 type_C; 2.
Pfam; PR00629; MAM; 1.
PRINTS; PR00020; MAMDOMAIN.
SMART; SM00431; FAS8C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103082 MW;
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PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS0072; FA58C_3; 2.
PROSITE; PS00740; MAM_1; 1.
PROSITE; PS50060; MAM_2; 1.
Anglogenesis; Transmembrane; Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF016296; AAC53337.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SMUUZJI, MAM; I.
SMART; SMO0137; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Matches 56; Conserv
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             55 NGSIHSPKFPHTYPRNWULVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635 NGTITTPGWPKEYPPNKNCVWQVVAPTQ-YRISMQF-EAFELEG--NEVCKYDYVEVRSG 690
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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8
                                                               POTENTIAL.
DORSAL-VENTRAL PATTERNING TOLLOID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
SIMILARITY)
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                                                                                                                                          METALLOPROTEASE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.4%; Score 174; DB 1; Length 1022;
41.7%; Pred. No. 2.7e-06;
tive 20; Mismatches 35; Indels
                                                                                                                                                                                           CUB 2.
BGF-LIKE 1, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                 CUB 3.
EGF-LIKE 2, CALCIUM-BINDING
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STRAIN-Sprague-Dawley;
MEDLINE-97433085; PubMed=9288754;
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16-OCT-2001 (Rel. 40, Last seq
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1022 AA; 115536
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MEDLINE-96353149; PubMed=8748368;

MEDLINE-96353149; PubMed=8748368;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Rawakami A., Kitsukawa T., Takagi S., Fujisawa H.;

Thorelopmentally regulated expression of a cell surface protein,

The mouse nervous system.";

The meuropilin, in the mouse nervous system.";

The meuropilin, in the mouse nervous system.";

The meuropilin, in the mouse nervous system.";

The production of a cell surface protein,

The production of a cell surface protein,

THE PLOSA SYSTEM, IN ANDIOGENESIS OUTSIDE THE NERVOUS SYSTEM, IT MEDIATES THE CHEMOREDUSANT ACTIVITY OF SEMARHORINS. IT BINDS TO SEMARHORIN 3A, THE PLGF-2 ISOFORM OF PGF, THE VEGF-165

TISOFORM OF VEGF-1N OVEGF-B. COEXPRESSION WITH KOR RESULTS IN INCREASED VEGF-165

THE MAY REGULATE VEGF-INDUCED ANGIOGENESIS (BY SIMILARITY).

THE SUMELLULAR LOCATION: Type I membrane protein.

THE SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

THE SIMILARITY: Contains 2 FS/8 type C domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BTML outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                             62 KEPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
                                                                                               GYPHSYHPSEKCEWLIQAPEPYQRIMINENPHFDLEDRD---CKYDYVEVIDGENEGGRL 99
               LLLGLLLLTSALAGORTGTRAESNLSSKLOLSSDKEONGVODPRHERVVTISGNGSIHSP 61
                                                7 LLCATLALALALALAG-----TIKIENPGYLTSP 42
                                                                                                                                                                 100 WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155
                                                                                                                                             120 LGRWCGSGTVPGKQTSKGNHIRIRFVSDBYFPSEPGFCIHYSIIM--PQVTET-TSPS 174
                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neuropilin-1 precursor (A5 protein).
                                                                                                                                                                                                                                                          923 AA
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InterPro; IPR0000859; CUB domain.
InterPro; IPR000421; FASE C.
InterPro; IPR000998; MAM_Gomain.
Pfam; PP00431; CUB; 2.
Pfam; PP00754; F5 F5 F5 F7 Pfam; PP00629; MAM; I
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SMART, SM0012, CUB, 2.
SMART, SM00131, PASSC, 2.
SMART, SM00137, MAM; 1.
PROSITE, PS01180, CUB, 2.
PROSITE, PS01285; FASSC_1; 2.
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P97333;
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62 KFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEV--EEPSDGSV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 WGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEIFKRGPECSQNYTAPT 155
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STRAINEWHIE LEGHORN; TISSUE=Embryonic brain;

MEDLINE=95124761; PubMed=7601310;

Takagi S., Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,

Fujisawa H.; Kasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,

Fujisawa H.; Assuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,

Fujisawa H.; Casuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,

Fujisawa H.; Rasuya M., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,

Fujisawa H.; Sasuya Y., Shimizu M., Matsuura T., Tsuboi M., Kawakami A.,

Fujisawa H.; RECEPTOR S.

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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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                                                                                                Glycoprotein; Neurone; Signal; Repeat;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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F5/8 TYPE C
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Neuropilin-1 precursor (A5 protein).
NRP1 OR NRP.
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                                                                                             Anglogenesis; Transmembrane;
PS01286; FA58C_2; 2
PS50022; FA58C_3; 2
PS00740; MAM_1; 1.
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265
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104
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923 AA;
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EMBL; M84144; AAA30072.1; -.
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P98068;
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                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 EV--EEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 EVIDGDNAEGRLWGKYCGK-IAPPPLVSSGPYLFIKFVSD-YETHGAGFSIRYEVFKRGP 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 IKILSPGYLTSPGYPQSYHPSQKCEWLIQAPEPYQRIMINFNPHFDLEDRD---CKYDYV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 QVTE--TTSPSVLP-----PSSLSLDL-----LNNAVTAFSTLEELIRYLEPD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 ECSRNFTSSSGMIKSPGFPEKYPNSLECTYIIFAPKMSBIILEFESFE-----LEPD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01180; CUB; 2.
PROSITE; PS01286; FA58C_1; 2.
PROSITE; PS01286; FA58C_2; 2.
PROSITE; PS00740; MAM 1; 1.
PROSITE; PS00740; MAM 2; 1.
PROSITE; PS0060; MAM_2; 1.
PROSITE; PS0060; MAM_2; 1.
Receptor; Cell adhesion.
                        -!- STBECLIGUAR LOCATION: Type I membrane protein.
-!- TISSUB SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
(LAYERS D AND E OF SGFS), AMACRINE CELLS OF RETINA, NEURITES OF
DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, B.G.
BLOOD VESSELS IN THE ENTIRE EMBRYO.
-!- SIMILARITY: CONTAINS TO THE NEUROPILIN FAMILY.
-!- SIMILARITY: COntains 2 E5/8 type C domains.
-!- SIMILARITY: Contains 1 MAM domain.
SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.0%; Score 167; DB 1; Length 914; 28.8%; Pred, No. 8.6e-06; tive 31; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
SIMILARITY.
DD2EEGD6F0CBB68C CRC64;
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F5/8 TYPE C 2.
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PROBABLE.
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InterPro; IPR000421; FAS8_C.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00431; CUB; 2. —
Pfam; PF00754; F5 F8 LYPe_C; 2.
Pfam; PF00629; MAM; 1.
PRINTS; PR00020; MAMDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102480 MW;
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                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
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PER SPRINGER OF STANDARD, PRT, 616 AA.

D. 10-TER-1996 (Rel. 33, Created)
D. 01-TER-1996 (Rel. 33, Created)
D. 10-TER-1996 (Rel. 33, Last esquence update)
D. 11-JUL 1998 (Rel. 34, Last amoration update)
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D. 12-JUL 1998 (Rel. 34, Last amoration update)
D. 13-JUL 1999 (Rel. 34, Last amoration update)
D. 15-JUL 1998 (Rel. 34, Last amoration update)
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Gaps 11;
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                                                                                                                                                                                                                                                                                                                                                                                               384 DMEIETETLCRYDAVEVRKDDINSIGEKFCGN-TLPPVQISSSNQMMVSFTSD---PSIT 439
                                                                                                                                                                                                                                                                                                                                                                       95 GLEDPEDDICKYDFVEVEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPS-- 152
                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                          94
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Jani-Sait S., Shows T.B., Greenspan D.S.;
"Type I procollagen COOH-terminal proteinase enhancer protein:
identification, primary structure, and chromosomal localization of the
cognate human gene (PCD.CE).";
J. Biol. Chem. 269:26280-26285 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hirahara I., Syoufuda K., Harada K., Tomita M., Urakami K., Terai H., Morisaki N., Salto Y., Morisaki N., Salto Y., "Smooth muscle cell derived procollagen C-protease enhancer protein."; cell Struct. Funct. 21:662-662(1996).
                                                                                                                                                                                                                                                                                       ------GSIHSPKFPHTYPRNMVLVMRLVAVDENVRIQLTFDERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last amotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I
procollagen COOH-terminal proteinase enhancer) (Type I proteinase enhancer protein).
                                                                                                                                                                                                        LTSALAGORTG-TRAESNLSSKLQLSSDKE-----QNGVQDPRHERVV--TISGN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                    Score 163.5; DB 1; Length 616;
Pred. No. 1e-05;
0; Mismatches 85; Indels 47;
    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRGFKATYVIIIQTTTVFSTTTLQTTPPSTTTLQTTNPSTTTLQT 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 EPGFCIHYSIIMPQVT--ETTSPSVLPPSSLSLDLLNNAVTAFST 195
                                                                                 397CD923FFB9EB98 CRC64;
ZINC (CATALYTIC) (
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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30; Mismatches
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MEDL TNE=95014462; PubMed=7523404;
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200
315
317
328
67902 MW;
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                                                                                                                          8.8%;
                                                                                                                                              28.0%;
                                                                                                                                              Similarity 28.09 S3; Conservative
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299 3
305 3
319 3
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SEQUENCE FROM N.A.
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Q15113; O14550;
30-MAY-2000 (Rel
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DT 30-MAY.
DT 10-SEP.
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RESUBLE-ETAIN;

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RESUBLE-ETAIN;

RESUBLE-ETAIN;

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RESUBLE-ETAIN;

RESUBLE R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Hahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20092917; PubMed=10625689;
Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.
                               Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S., "Structural organization and expression patterns of the human and mouse genes for the type I procollagen COOH-terminal proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 600270; -.
GO; GO:0008151; P:cell growth and/or maintenance; TAS.
GO; GO:0007275; P:development; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, 133799, AAA61949.1; ALT_SEQ.
EMBL, AB008549; BAA23281.1; -.
EMBL, AF083356; AAC78800.1; -.
EMBL, AF083655; AAD16041.1; -.
EMBL; BC000574; AAH06574.1; -.
EMBL; BC033205; AAH33205.1; -.
MEDLINE=99134301; PubMed=9933570;
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InterPro, IPR001134; Netrin_C.
                                                                                                                                                                                          Genomics 55:229-234 (1999).
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Pfam; PF01759; NTR; 1.
SMART; SM00643; C345C; 1.
SMART; SM00042; CUB; 2.
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                                                                                                                                                      enhancer protein."
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DOMAIN
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DISULFID
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ID NRP2_H

C 06.0452 H

T 06.0472 H

DT 16.0CT

DT 28.PEB-

DF Neuropi

DE Neuropi

DB Neuropi

GN NRP2 OF

OC BUMO 88

OC MARMATIVI

OC MARMATIVI
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                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                   56 GSIHSPKFPHT-YPRNMVLVWRLVAVDENVRIQLTFDBRFGLEDPEDDICKYDFVEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                         112 BEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM----- 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYKTLPRGTAKEG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ginty D.D.;
"Neuropilin is a semaphorin III receptor.";
"Neuropilin is a semaphorin III receptor.";
"Neuropilin is a semaphorin III receptor.";

-I- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
-I- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
-I- FUNCTION: HIGH AFFINITY RECEPTOR NOT THE PROFILE PROFILED FOR PROFILE SUBCLIFICITY: FOUND IN GERTAIN NEURONAL POPULATIONS OF THE CNS AND IN OTHER NONNEURONAL TISSUES INCLUDING MESENCHYMAL TISSUE LINING IN THE RIBS. TO THE METER THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE PROFILE THE P
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                         8.5%; Score 158; DB 1; Length 449;
34.5%; Pred. No. 1.9e-05;
Ative 21; Mismatches 50; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Newropilin-2 precursor (Vascular endothelial cell growth factor 165 receptor 2).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                            POTENTIAL.
PROCOLLAGEN C-PROTEINASE ENHANCER
PROTEIN.
                                                                                                                                                                                                                                                                           -LINKED (GLCNAC. . .) (PC
3D88430158648796 CRC64;
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-!- SIMILARITY: Contains 2 CUB domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 1 MAM domain.
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                                                                                                   CUB 1.
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MEDLINE=97433085; PubMed=9288754;
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                                                                                                                                                                                                                                                                                        47972 MW;
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                48; Conservative
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22888
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2000
                         Glycoprotein; Repeat;
SIGNAL 1 25
CHAIN 26 449
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449 AA;
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Best Local Similarity
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CARBOHYD
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42 QDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLFFDERFGLEDPED 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 -- CKYDFIEIRDGDSESADLLGKHCGN-IAPPIISSGSVLYIKPTSD-YARQGAGFSLR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 QDPPCGGRINSKDAGYITSPGYPQDYPSHQNCEWVVYAPEPNQKIVLNFNPHFEIEKHD-
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060452; 014820; 014821;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last amonotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
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103896 MW; 3BF62903F644851C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
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F5/8 TYPE C 1.
F5/8 TYPE C 2.
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N-LINKED (GLCNAC. . . )
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33.3%; Pred. No. 7.5e-05;
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tive 19; Mismatches
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or send an email to license@isb-sib.ch)
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InterPro; IPR000859; CUB domain.
InterPro; IPR000859; MAM domain.
Fram; PP00431; CUB; 2.
Fram; PP00431; CUB; 2.
Fram; PP00529; MAM J.
FRINTS; PR00020; MAMDOMAIN.
SWART; SM00442; CUB; 2.
SWART; SM00142; CUB; 2.
SWART; SM00131; FASSC; 2.
FROSITE; PS01180; CUB; 2.
FROSITE; PS01286; FASSC_1; 2.
FROSITE; PS01286; FASSC_2; 2.
FROSITE; PS01286; FASSC_2; 2.
FROSITE; PS01286; FASSC_2; 2.
FROSITE; PS01286; FASSC_2; 2.
FROSITE; PS01286; FASSC_2; 2.
FROSITE; PS00022; FASSC_2; 2.
FROSITE; PS00022; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
FROSITE; PS00021; FASSC_2; 2.
                                                EMBL; AF016297; AAC53338.1; -.
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NRP2 OR VEGF165R2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20309748; PubMed=10748121;
MEDLINE-20309748; PubMed=10748121;
MEDLINE-20309748; PubMed=10748121;
MILLINE-20309748; PubMed=10748121;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Town of vascular endothelial growth factor (VEGF) and of placenta growth factor 2, but only neuropilin-2 functions as a receptor for the 145-amino acid form of VEGF.";
J. Biol. Chem. 275:18040-18045(2000).
J. Biol. Chem. 275:18040-18045(2000).
J. Biol. Chem. 275:18040-18045(2000).
J. Biol. Chem. 275:18040-18045(2000).
MUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN 3C RECEPTOR.
C. I- SUBCELLULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97470888; PubMed-9331348; Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.; Neurcopilin-2, a novel member of the neurcopilin family, is a high affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                                                                                                                                                                                                                                                                                                                          Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M., "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; cell 92:335-745(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=060462-3; Sequence=VSP_004341;
-!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-!- SIMILARITY: Contains Z UB domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
Name=A22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=060462-2; Sequence=VSP_004342;
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                                                       SEQUENCE FROM N.A. (ISOFORMS AO AND A17).
                                                                                                                                                                                                                                                                                                                                      TISSUE=Breast;
MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM A22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF022859; AAC51788.1; -.
EMBL; AF022860; AAC51789.1; -.
EMBL; AF016098; AAC12922.1; -.
HSSP; P12259; 1CZT.
Genew; HGNC; 8005; NRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00020; MAMDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00042; CUB; 2.
SMART; SM00231; FASSC; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                                          Neuron 19:547-559(1997).
[2]
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16 SRHQVRGQPDPPCGGRLNSKDAGYITSPGYPQDYPSHQNCEWIVYAPEPNQKIVLNFNPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 SDKEQNGVQDPRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-57470888; PubMed=9331348; Chen H.; Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.; "Neuropilin-2, a novel member of the neuropilin family, is a high affinity receptor for the semaphorins Sema B and Sema IV but not Sema III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
WRP2_MOUSE STANDARD; PRT; 931 AA.
035375; 035373; 035374; 035376; 035377; 035378;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165 NRP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          POLY-SER.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 8.4%; Score 155.5; DB 1; Length: Similarity 32.1%; Pred. No. 7.6e-05; A2; Conservative 20; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> K (IN REF. 1).
270CBAE69A0A797C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform Al7).
/FTId=VSP_004341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (in isoform A0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           004342.
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F5/8 TYPE C 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104830 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        809
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786 71
931 AA;
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
838
838
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ID VEGD_RAT
AC 035251;
                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                       DISULFID
                                                                            CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                           VARSPLIC
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                                                                                                                                                VARSPLIC
                                                                                                                                                                       VARSPLIC
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                                 DISULFID
                                             DISULPID
                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                ISOId=035375-6; Sequence=VSP 004347;
-!- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES, INTERIAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES, INTERIAL ENTHELIUM, KIDNEY, LUNG AND SUBMANDIBULAR GLAND.
-!- DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS DEVELOPMENTALLY REGULATED.
-!- SIMILARITY: COntains 2 CUB domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 1 MAM domain.
          -i- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOFORM OF VEGF, AND THE PIGF-2 ISOFORM OF PGF.
-i- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
-i- SUBCELLUIAR LOCATION: Type I membrane protein.
-i- ALTERNATIVE PRODUCTS:
-i- ALTERNATIVE PRODUCTS:
-i- SPERIALIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R Pfam; PF00431; CUB; 2.

R Pfam; PF00431; CUB; 2.

R Pfam; PF00431; CUB; 2.

R PRINTS; PR00020; MAM; 1.

R SMART; SM00042; CUB; 2.

R SMART; SM00137; MAM; 1.

R PROSITE; PS01285; FAS8C; 2.

R PROSITE; PS01285; FAS8C_1; 2.

R PROSITE; PS01285; FAS8C_2; 2.

R PROSITE; PS01285; FAS8C_2; 2.

R PROSITE; PS0066; MAM 2; 1.

R PROSITE; PS0066; MAM 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROPILIN-2.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CUB 1.
CUB 2.
F5/8 TYPE C 1.
F5/8 TYPE C 2.
MAM.
                                                                                                                           IsoId=035375-2; Sequence=VSP_004344;
                                                                                                                                     Name=A5;
IsoId=035375-3; Sequence=VSP_004345;
                                                                                                                                                                      IsoId=035375-4; Sequence=VSP_004343;
                                                                                                                                                                                              IsoId=035375-5; Sequence=VSP_004346;
                                                                                                    IsoId=035375-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AF022856, AAC53379.1; --
EMBL, AF022854, AAC53377.1; --
EMBL, AF022855, AAC53378.1; --
EMBL, AF022857, AAC53380.1; --
EMBL, AF022861, AAC53381.1; --
EMBL, AF022861, AAC53381.1; --
HSSP; P12259; LCZT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1100492; Nrp2.
InterPro; IPR000859; CUB domain.
InterPro; IPR000421; FA58 C.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing.
SIGNAL 21
CHAIN 21 931
DOMAIN 21 864
TRANSMEM 865 889
DOMAIN 890 931
DOMAIN 149 267
DOMAIN 277 427
DOMAIN 642 802
 19:547-559(1997)
                                                                                            Name=A22;
                                                                                                                                                            Name=A17
                                                                                                                 Name=A0;
                                                                                                                                                                                                          Name=B5;
                                                                                                                                                                                   Name=B0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKSMIXTLDPILITIIAMSSLGVLLGATCKGLLLYCTCSYS
GLSSRSCTLENYMFLYDGLKHYKKINHQKCCGEA -> G
GLPPPGTEPTUTUVVQPIPAYWYYWAAGGAVLVLASVVL
ALVLHYHRRYAAAKTDHGITYKTGHYTNGAPLAVEPTLTI
KLEQERGSHC (1n isoform B5).
//FTLd=vSP 004347.
//FTLd=vSP 004347.
104558 MW; 76F2443F411D2F63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDFKVDIPETHGGEGYEDBIDDEYEGDWSNSSSTSGAGDP
SSGKEKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCT
CSYSGLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -> GTLPPGTEPTUDTVPVQPIPAYMYYWMAAGGAVLVLAS
VVALAVLHYRRFRYAMKTDHSITYKTSHYTNGAPLAVEPT
LTIKLEQERGSHC (in isoform B0).
/FTId=VSP_004346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
48-SEP-2003 (Rel. 42, Last annotation update)
48-SEP-2003 (FIGF)
48-SEP-2003 (FIGF)
58-SEP-2003 (FIGF)
69-SEP-2003 (FIGF)
69-SEP-2003 (FIGF)
69-SEP-2003 (FIGF)
69-SEP-2003 (FIGF)
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69-SEP-2003 (FIGF
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Yamada Y., Hirata Y., Nezu J., Shimane M.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Growth factor active in angiogenesis, lymphangiogenesis and endothelial cell growth, stimulating their proliferation and migration and also has effects on the permeability of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria; Rođentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
MISSING (In isoform Al7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform A0).
/FTId=VSP_004344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (In isoform A5). / FTId=VSP_004345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.4%; Score 155.5; DB 1
32.8%; Pred. No. 7.6e-05;
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                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
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vessels. May function in the formation of the venous and lymphatic vascular systems during embryogenesis, and also in the maintenance of differentiated lymphatic endothelium in adults. Binds and activates VEGRR-3 (Flt4) receptor (By similarity).

-!- SUBCELULIAR LOCATION: Secreted (By similarity).

-!- PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGRR-3 and VEGRR-2. VEGR-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGRP is composed mostly of two VEGR homology domains (VHDs) bound by non-covalent interactions (By similarity).

-!- SIMILARITY: BELONGS TO THE PDGF/VEGR FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263
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PROSITE; PS00249; PDGF_1; 1.

PROSITE; PS50278; PDGF_2; 1.

Angiogenesis; Micogen; Growth factor; Glycoprotein; Signal; Repeat;

Angiogenesis; Micogen; Growth factor; Glycoprotein; Signal; Repeat;

Angiogenesis; Micogen; Growth factor; POTENTAL.

POTENTIAL.
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HSSP; P15692; 1VPP.
InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF03128; CXCXC; 1.
Pfam; PF03128; CXCXC; 1.
ProDom; PD001629; PD_growth_factor; 1.
SMART; SM00141; PDGF; 1.
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Best Local Similarity 27.7*
Matches 56; Conservative
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-- PELVPVKIANHTGCKCLPTG 200

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Search completed: November 25, 2003, 21:02:52 Job time : 9.55655 secs

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; Search time 30.4613 Seconds (without alignments)
2922.663 Million cell updates/sec
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                                                                                                                                                                                                                                     1 MLLLGLLLTSALAGQRTGT.....DVALEHHEECDCVCRGNAGG 345
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GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    830525 segs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                 November 25, 2003, 20:58:59
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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	ai .	Q9QY71	Q8CI19	Q9JHV8	Q9EQX6	Q9UL22	Q9NRA1	Q91946	Q8K429	Q9EQT1	Q9GZP0	Q9BWV5	092517	Q8K2L3	QBQFX6	OBAXP1	057658
	В :	11	11	11	11	4	4	13	11	11	4	4	11	11	13	13	13
% Query	Length	345	345	345	345	345	345	345	258	370	370	364	370	261	923	923	691
% Query	Match	100.0	6.66	98.4	97.5	90.2	0.06	84.0	74.4	40.8	40.7	40.6	40.4	23.8	10.9	10.9	10.4
	Score	1848	1846	1819	1801	1667	1664	1552	1375	754	752	750.5	746.5	440.5	201	201	192.5
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34 1	977 1	735 1	926 4	1015 4	1012 1	241 1	609	644 4	704 4	1007	3623 4	1008 1	921 1	1013 1	1019 1	1013 4	1013 4	919 1	936 1	3623 1	145 1	926 1	3620 6	276 4	415 4	555 4	901 4	901 4
10.4	10.3	10.1	10.0	10.0	6.6	8.6	9.5	9.5	9.5	9.5	4.6	9.1	9.1	6.8	8.9	8.8	8.8	8.7	8.7	8.7	9.8	9.8	8.5	8.5	8 .5	8.4	8.4	8.4
192	191	186	185	185	183	181	176	176	176	175	174.5	169	168	165	165	162	162	161.5	161.5	160	158.5	158.5	158	157	157	155.5	155.5	155.5
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## ALIGNMENTS

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RESULT 1

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DO 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DO 10-MAY-2000 (TrEMBLrel. 23, Last annotation update)

DO 10-MAY-2000 (TrEMBLrel. 23, Last annotation update)

DO 10-MAY-2000 (TrEMBLrel. 23, Last annotation update)

DO 10-MAY-2000 (TrEMBLrel. 23, Last annotation update)

Enloctin (Platelet-derived growth factor C).

GN Mus musculus (Mouse).

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241 LKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
                                                                                                                                                                                                                                                                                                 241 LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
   PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDLCKYDFVEVEFEPSDGSVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-Swiss-Webster/NIH;
MEDLINE-20417814; PubMed=10960785;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
"The mouse Pdgfc gene: dynamic expression in embryonic tissues during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GRWCGSETVPGKQTSKGNHIRIRFVSDEYFPSEPGFCHYSIIMPQVTETTSPSVLPPSS
                                                                GRWCGSGTVPGKOTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                              121 GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEFGFCIHYSIIMPQVTETTSPSVLPPSS
                                                                                                                                                                                181 LSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNL
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 38886 MW; FA1486BED6D362F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
platelet-derived growth factor C.
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Pred. No. 1.2e-163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 341; Conserv
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1848; DB 11; Length 345; 100.0%; Pred. No. 2.2e-166; ive 0; Mismatches 0; Indels 0;
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EMBL; AK033734; BAC28455.1; -.
EMBL; AK042767; BAC31358.1; -.
EMBL; AK052947; BAC31358.1; -.
EMBL; AK052947; BAC3516.1; -.
MGD; MG11859631; PG45.1; -.
InterPro; IPR0000859; CUB domain.
InterPro; IPR0000859; CUB, 1.
EFan; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS07180; CUB; 1.
PROSITE; PS07180; CUB; 1.
SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Strausberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037656; AAH37696.1; -.
SEQUENCE 345 AA; 38741 MW; 9A58A05C6C0E9614 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Platelet-derived growth factor, C polypeptide.
Mus musculus (Mouse).
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Best Local Similarity 100.
Matches 345; Conservative
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NCBI_TaxID=10090;
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Q8C119;
01-MAR-2003
01-MAR-2003
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hes 344;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                            301 VIKKYHEVLQLRPKTGVKGLHKSLTDVALEHHEECDCVCRGNAGG 345
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PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;
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Last annotation update)
                                                                                                                                                                                            345 AA
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Matches 334; Conservative
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01-MAR-2001
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MEDLINE=21347863; PubMed=11297552;

MEDLINE=21347863; PubMed=11297552;

A Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Paledhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;

Teldhaus A.L., Humes J.M., Palmer T.E., Hart Growth Factor That Binds to PDGF alpha and bata Receptor.";

J. Biol. Chem. 276:27446-2744(3201).

EMBL, AR091434; AAF00049.1;

EMBL, AR091434; AAF00049.1;

EMBL, AR26738; AAK51637.1;

InterPro; IPR000072; PD Growth factor.

PR InterPro; IPR000072; PD Growth factor.

PR Fam; PF00431; CUB; 1.

PR SWART; SM0042; CUB; 1.
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Hamada T., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique
member of the PDGF/VEGF family.";
FEBS Lett. 475:97-102(2000).
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                                                                                                    (SPINAL CORD-derived
                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                   TBai Y.J., Lee R.K.K., Lin S.P.;
"Fallotein, a novel growth factor like gene identified in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Scretcry growth factor-like protein FALLOTBIN (SPII)
growth factor) (Platelet-derived growth factor C).
HSCDGF OR PDGFC.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (Drownan)
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                                 VIKKYHEVLQLRPKTGVRGLHKSLIDVALEHHEECDCVCRGSTGG 345
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nat. Cell Biol. 2:302-309(2000).

-1-SIMILARITY: CONTAINS 1 CUB DOMAIN.

EMBL; AF244813; AAF80597.1; -.

Genew, HGNC:8801; PDGFC.

InterPro; IPRO00085; CUB domain.

InterPro; IPRO00085; PD_growth_factor.

Pfam; PF00431; PDGF; 1.

SMART; SM00141; PDGF; 1.

SMART; SM00142; CUB; 1.

SMART; SM00142; CUB; 1.

SMART; SM0180; CUB; 1.

SMART; SM0180; CUB; 1.

SMART; SM0180; CUB; 1.

SMART; SM0180; CUB; 1.

SRQNER; PS01180; CUB; 1.

PROSITE; PS01180; CUB; 1.

SRQUENCE 345 AA; 39043 MW; 590889CEAS5CC5EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.0%; Score 1664; DB 4; Length 3 Best Local Similarity 86.7%; Pred. No. 5.7e-149; Matches 299; Conservative 28; Mismatches 18; Indels
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                                                                                                                                                                                                                                            345 AA
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MEDLINE=20268201; PubMed=10806482;
                                                                                                                                                                                                                                        PRELIMINARY;
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Q91946
ID Q9194
AC Q9194
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STRAIN=white legions, TISSUE=Spinal cord;

WEDLINE=20317014; PubMed=10858496;

MEDLINE=20317014; PubMed=10858496;

Hamada T., Ui-Tein K., Miyata Y.;

Hamada T., Ui-Tein K., Miyata Y.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 PKFPHTYPRNTVLVWRLVAVDENVWIQLTFDERFGLBDPEDDICKYDFVEVEBFBGGTVL 120
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                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
Platelet-derived growth factor C (Fragment).
Rattus norvegious (Rat).
Bukarryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal cord-derived growth factor.
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84.0%; Score 1552; DB 13;
Best Local Similarity 80.3%; Pred. No. 2.3e-138;
Matches 277; Conservative 37; Mismatches 31;
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42 ESNHLTDLYRRDENIRVIGTGHVQSPRFPNSYPRNLLLTWRLHS-QEKTRIQLAFDHQFG 100
                                                                                                                                                     96 LEDPEDDICKYDFVEVEEPSDGS--VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE 153
                                                                                                                                                                                                    154 PGFCIHYSII---MPQ-----VTET-----TSPSVLPPSSLSLDLLNNAVTAFST 195
                                                                                                                                                                                                                                                                                         220 VEDLIKYFNPASWQDDLENLYMDTPRYRGRSY-HERKSK-VDLDRINDDVKRYSCTPRNH 277
                                                                                                                                                                                                                                                                                                                                        256 SVSIRBELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRKVTKKYHEVLQLRP-- 313
                                                                                                                                                                                                                                                                                                                                                        278 SVNLREBELKLINAVFFPRCLLVQRCGGNCGCGTLNWKSCTCSSGKTVKKYHEVLKFEPGH 337
                                                                  37 EQNGVQD-PRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFG 95
                                                                                                                                                                                                                                                                     196 LEBLIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKVVNLNLLKEBVKLYSCTPRNF
                                                                                                                                                                                                                        161 PGFKIYYSFVEDFQPEAASEINWESVTSSFSGVSYHSPSVM-DSTLTADALDKAIAEFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu B., Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S., Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J., Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q. Yuan J.G., Liew C.C., Zhao M.S., Hui R.T., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OGGZPO;
01-MMR-2001 (TrEMBLrel. 16, Created)
01-MMR-2001 (TrEMBLrel. 16, Last sequence update)
01-MMR-2003 (TrEMBLrel. 23, Last annotation update)
SPINAL CORP-defived growth factor-B (MSTP036) (IRIS-expressed growth
factor long form) (Platelet-derived growth factor D).
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PubMed=11331881;
Bergsten E., Uutela M., Li X., Pietras K., Ostman A., Heldin C.H.,
Alitalo K., Eriksson U.;
"PDGF-D is a specific, protease-activated ligand for the PDGF beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          List SEQUENCE FROM N.A.
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
Hamada T., Ui-Tei K., Imaki J., Miyata Y.;
"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/PDGF-C/fallotein.";
Blochem. Blophys. Res. Commun. 0:0-0(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                   28;
40.8%; Score 754; DB 11; Length 370; 46.2%; Pred. No. 8.5e-63;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
            46.2%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                            338 FKRRGKAKNMALVDIOLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor.";
Nat. Cell Biol. 3:512-516(2001)
                 Best Local Similarity 46.29
Matches 151; Conservative
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   Query Match
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Q9GZP0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGKAFLYGKKSKVVNINLLKEEVKLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 LLGKAFLYGKKSKAVNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCG 240
                                                                                                                                                                                                                                                                                                                                                                                                                       DICKYDFVEVEEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCHYS 161
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MEDLINE=21092670; PubMed=11162582;
MEDLINE=21092670; PubMed=11162582;
MEDLINE=21092670; PubMed=11162582;
MEDLINE=21092670; PubMed=11162582;
MEDLINE=21092670; PubMed=11162582;
MOGENIAR TY: CONTAINS 1 COMMIN. 280:733-737(2001).

LISTICARLY: CONTAINS 1 COMMIN. 280:733-737(2001).

-1-SIMILARRY: CONTAINS 1 COMMIN. 280:733-737(2001).

REMBL; ABOS170; BAB18920.1; -

IN THEFPTO; IPRO00072; PD_GTOWTh. factor.

REMR; SM00041; CUB; 1.

SMART; SM00141; POGF; 1.

PROSITE; PSS01180; CUB; 1.

PROSITE; PSS01180; CUB; 1.

PROSITE; PSS0278; PDGF_2; 1.

PROSITE; PSS0278; PDGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal-cord derived growth factor-B.
RSCDGF-B.
RACUBE norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                      ;
STRAIN=Sprague-Dawley; TISSUE=Skin;
Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
"Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
                                                                                                                                                                                                                                                                                Score 1375; DB 11; Length 258;
Pred. No. 8.6e-122;
5; Mismatches 3; Indels 0
                                           Healing.";
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, SIMILARITY. CONTAINS 1 CUB DOMAIN.
EMBL, AFS08348; AAM47265.1; -...
InterPro; IPR000859; CUB domain.
InterPro; IPR00431; CUB; 1...
Ffan; PF00431; CUB; 1...
PROSTITE; PS01180; CUB; 1...
PROSTITE; PS0278; PDGF_2; 1...
                                                                                                                                                                                                                                                    258 AA; 29255 MW; 88625B989FCC3F8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNCACCLHNCNECOCVPR 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.48;
                                                                                                                                                                                                                                                                                                                     Matches 250; Conservative
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                                                                                                                                                                                                                                                                                                     Local Similarity
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Q9EQT1
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SEQUENCE FROM N.A.

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SEQUENCE FROM N.A.
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MEDLINE=21231380; PubMed=11331882;
LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,
A himkets R.A., Rothberg J.M., Lichenstein H.S.;
T. PDGF D. A Novel Protease-Activated Growth Factor.";
T. Lak. Cell Biol. 3:517-521(2001).
T. SIMILARITY: CONTAINS 1 CUB DOWAIN.
BEBL; AR13326; AA8392871; -.
EMBL; AR03332; BAB18903.1; -.
BEBL; AR035584; AAK58840.1; -.
BEBL; AR35584; AAK58840.1; -.
BEBL; AR35584; ARX88840.1; -.
BEBL; AR35584; ARX88840.1; -.
BEBL; AR000072; PD_Growth_factor.
RINterPro; IRRO00031; TomB_boxC.
BEAM: PRO0431; CUB; 1.
BEAM: SWART; SM00043; CUB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVNIRBELKCLANVVFFFRCLLVQRCGGGCGTVNWRSCTCNSGKTVKKYHEVLQFEPGH 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEDPEDDICKYDFVEVEEPSDGSVL--GRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQNGVQD - PRHERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFG
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pgfkiyysiledfqpaaasetnwesvtssisgvsynspsvtdp-tliadaldkkiaefdt
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-UTN-2001 (TrEMBLrel. 17, Last sequence update)
01-UN-2001 (TrEMBLrel. 23, Last annotation update)
17:1s-expressed growth factor short form (Spinal cord-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.7%; Score 752; DB 4; Length 37
45.3%; Pred. No. 1.3e-62;
cive 59; Mismatches 92; Indels
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Stomitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01180; CUB; 1.
PROSITE; PS00278; PDGE 2; 1.
PROSITE; PS00430; TONB_DERENDENT_REC 1; 1.
SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 2), Last annotation update)
Platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109
product:platelet-derived growth factor D).
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MEDLINE=12231380; PubMed=11331882;
MEDLINE=12231380; PubMed=11331882;
MEDLINE=1231380; PubMed=11331882;
Giase N.A., Jokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C., Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J., Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D, A Novel Protease-Activated Growth Factor.";
Nat. Cell Biol. 3:517-521(2001).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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40.6%; Score 750.5; DB 4; Length 364;
Best Local Similarity 45.6%; Pred. No. 1.8e-62;
Matches 145; Conservative 58; Mismatches 88; Indels 27;
TISSUE=Testis;
Strausberg R.;
Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; A7027518; AAK20082.1; -.
R EMBL; BC030645; AAH30645.1; -.
R InterPro; IPR000053; CUB domain.
InterPro; IPR0000531; TonB boxC.
R InterPro; IPR000531; TonB boxC.
R Pfam; PF00431; CUB; 1.
R PROSITE; PS01180; CUB; 1.
R PROSITE; PS01180; CUB; 1.
R PROSITE; PS00430; TONB DEPENDENT REC 1; 1.
R PROSITE; PS00430; TONB DEPENDENT REC 1; 1.
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341 MALVDIQLDHHERCDCIC 358
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Body;
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the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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SETRAIN=CS7BL/G4, TISSUE=Body;
MEDLINE=CS7BL/G409374; PubMed=1042159;
CAZALING: P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muřamatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Fori F., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Saito H., Saaito R., Sakai K., Sano H., Saaski D., Shibata K., Shibata X., Shinagawa A., Shiraki T., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshido K., Yoshino M., Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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STRAT=C5PHL/61; TISSUE=Body;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Natsuhiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
*RIKEN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
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370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Rayashizaki Y.;
"High-efficiency full-length conn.";
Meth. Enzymol. 303:19-44(1999).
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InterPro; IPR000072; PD_Growth_factor.
Pfam; PF00431; CUB; 1.
SMART; SM00042; CUB; 1.
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EMBL; AF335583; AAK38839.1; -.
EMBL; AK003359; BAB22735.2; -.
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MEDLINE=22354683; PubMed=12466851;
The PANTOM Consortium,
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MEDLINE-21085660; PubMed=11217851;
RIKEN PANTOM Consortium;
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PROSITE; PS50278; PDGF 2;
SEQUENCE 370 AA; 42809
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40.4%; Score 746.5; DB 11; Length 370; 43.5%; Pred. No. 4.4e-62;

Best Local Similarity

Ouery Match

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201 TDP-TLTADALDKTVABFDTVEDLLKHFNPVSWQDDLENLYLDTPHYRGRSY-HDRKSK- 257
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                                                                                                                                                                                                                 176 LPPSSLSLDLLINNAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKV 235
                                                                                                                                                                                                                                                                                                                                                 236 VNLNLLKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQ 295
                                                                                                                                                                                                                                                                                                                                                                     134 ISKGNHIRIRRVSDEYFPSEPGFCIHYSII---MPQVTETT-----SPSV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 LPPSSLSLDLLANAVTAFSTLEELIRYLEPDRWQVDLDSLYKPTWQLLGKAFLYGKKSKV 235
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                                                                                                                 76 RLVAVDENVRIQLIFDERFGLEDPEDDICKYDFVEVEPEPSDGS--VLGRWCGSGTVPGKQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 RLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEREPSDGS--VLGRWCGSGTVPGKQ 133
                                                         26 QRASIKALRNAN----LRRDESNHLTDLYQREENIQVTSNGHVQSPRFPNSYPRNLLLTW 81
                                     16 ORIGIRAESNISSKIQLSSDKEQNGVODPRHERVVTISGNGSIHSPKFPHTYPRNMVLVW 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 QRASIKALRNAN----LRRDESNHLTDLYQREENIQVTSNGHVQSPRFPNSYPRNLLLITW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ORTGTRAESNLSSKLOLSSDKEONGVODPRHERVVTISGNGSIHSPKFPHTYPRNMVLVW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.8%; Score 440.5; DB 11; Length 261;
38.7%; Pred. No. 2.5e-33;
Live 49; Mismatches 73; Indels 27; Gaps
63; Mismatches 102; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                             296 CVPRKVTKKYHEVLQLRP---KTGVKGLHKSLTDVALEHHBECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 CSSGKTVKKYHEVLKFEPGHFKRRGKAKNMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2009 (TrEMBLrel. 23, Last annotation update)
Similar to platelet-derived growth factor, D polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Strausberg R.; Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (UUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; EC030896; AAH30896.1; -. MGJ) WGRI:1919035; Pdgfd. InterPro; IPR00859; CUB_domain. PF00431; CUB; 1. PROSITE; PR00421; CUB; 1. SEQUENCE 261180; CUB; 1. SEQUENCE 261 AA, 30228 MW; ZEEC3F6373A52D09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94; Conservative
    Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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236 VNL 238

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61 PKFPHTYPRINMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEVEEPSD--GS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 LVGKYCGK-IAPSPVVSSGNQLFIKFVSD-YETHGAGFSIRYEIFKTGPECSRNFTSSSG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLLLGLLLLTSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;

Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;

Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;

"Neuropiln." is required for normal vascular development and is a mediator of VEGF-dependent angiogenesis in zebrafish.";

L. Submitted (NOV-2001) to the EMBL/Genbank/DDBJ databases.

C. SUMILARITY: BELONGS TO THE NEUROPILIN FAMILY.

C. SIMILARITY: CONTAINS 1 WAM DOWAIN.

C. SIMILARITY: CONTAINS 1 FF/8 TYPE C DOWAIN.

C. SIMILARITY: CONTAINS 1 FF/8 TYPE C DOWAIN.

DR EMBL: AVG6421; ALLG08621; -..

DR EMBL: AVG6421; ALLG08621; -..

DR EMBL: AVG6421; ALLG08621; -..

DR FEAM: PRO00389; CUB domain.

DR InterPro: IPR000989; WAM domain.

DR Pfam: PR00431; CUB; 2.

DR Pfam: PR00431; CUB; 2.

DR Pfam: PR00431; CUB; 2.

DR SWART: SM0044; CUB; 2.

DR SWART: SM00421; FA58C; 2.

DR SWART: SM00421; FA58C; 2.

DR SWART: SM00431; FA58C; 2.
                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 VIKSPGFPEKYPNNLDCTFMIFAPKMSEIVLEFESFE----LEPD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C 1; 1.
PROSITE; PS001286; FA58C 2; 2.
PROSITE; PS001280; MAM_I; 1.
PROSITE; PS50060; MAM_I; 1.
Glycoprotein; Receptor; Transmembrane.
SEQUENCE 23 AA: 102492 MW; 2ED84B129AA92B2D CRC64;
                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                            NCBI_TaxID=7955;
259 IEV 261
                                                                                                                                                                                             Neuropilin-1.
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                                                                                              Q8QFX6
                                                Matches
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74; Indels 58; Gaps 10;

Length 923;

Search completed: November 25, 2003, 21:04:35 Job time : 31.4613 secs

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61 PKFPHTYPRNMVLVWRLVAVDENVRIQLTFDERFGLEDPEDDICKYDFVEVEEFSD--GS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 VLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHYSIIM--PQVTE--TT5PS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 PGYPVSYYPSQKCIWVITAPGPNQRILINFNPHFDLEDRE----CKYDYVEVRDGVDENGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MILLIGLILLITSALAGQRTGTRAESNLSSKLQLSSDKEQNGVQDPRHERVVTISGNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 ILFTGIFLIVSALKNDKCGDN.------IRITSANYLTS 39
                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Indels 58; Gaps
                                                                                 Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.9%; Score 201; DB 13; Length 923; Best Local Similarity 27.9%; Pred. No. 6.5e-10; Matches 63; Conservative 31; Mismatches 74; Indels 5E
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                                                                                                                                                                                                                                             Shoil W., Tawarayama H.;
The cloning and expression of neuropilin-1.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AB088776; BAC53657.1;
SEQUENCE 923 AA; 102541 MW; 0E6CE33ED28A21F7 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=7955;
                                               Neuropilin-1.
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